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;
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 945 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
;
US-08-867-087B-10

Query Match      10.6%; Score 92.2; DB 2; Length 945;
Best Local Similarity 67.4%; Pred. No. 1.1e-16;
Matches 130; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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Db 16 ATGGGAAGGGGTAGGGTTGAGCTTAAGAGAAATAGAGAACTCAAGGCGAAGTGAAC 75
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QY 181 TCAACTACGCTGA 193
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RESULT 9
US-08-592-214A-7
; Sequence 7, Application US/08592214A
; Patent No. 581536
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,214A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1927
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

;
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 945 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
;
US-08-592-214A-7

Query Match      10.6%; Score 92; DB 1; Length 1345;
Best Local Similarity 48.5%; Pred. No. 1.6e-16;
Matches 294; Conservative 0; Mismatches 300; Indels 12; Gaps 1;

QY 1 ATGGGACGTGGGAGGTTGAGATCAAGAGGATTGAGAACTCAAGTCAAGGCGAGGTGACC 60
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Db 269 GCGGAGGTGCGCGTCACTGCTCTCTCCCGCAAGGCGAAGCTCTACGAGTACGCCACCGAC 328
QY 181 TCAACTACGCTGACAGAAATCTTGGACAA-----ATACCTGGACAATCTGG 228
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QY 229 AAGAAGTTGTGGGATGCTAAGCATGAGAACTCTCAGCAATGAAGTGGATAGAGTCAAGAA 288
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QY 409 GACAAAGCAGTCCAAAGTTGCTGACATGATGAGAGCAATGGAAGGCACTGGAAGATGAG 468
Db 569 TCAAGGAGAGGCCACCTTATGGCCAGTCTATTTCTGAGCTACAGAGAGGAGGTCA 628
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Db 749 CAGACA 754

RESULT 10
US-08-659-188-7
; Sequence 7, Application US/08659188
; Patent No. 6002069
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; TITLE OF INVENTION: Reproductive Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
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/ ZIP: 92122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/659,188
/ FILING DATE: 05-JUN-1996
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-UD 1946
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1345 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 149..968
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 1..1345
/ OTHER INFORMATION: /note= "product = Zea mays AP1."
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/ US-08-659-188-7
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/ Query Match 10.6%; Score 92; DB 3; Length 1345;
/ Best Local Similarity 48.5%; Pred. No. 1.6e-16;
/ Matches 294; Conservative 0; Mismatches 300; Indels 12; Gaps 1;
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/ QY 1 ATGGGAGCTGGGAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACAGGAGGTCACC 60
/ Db 149 ATGGGCGCGGAGGTACAGTCAAGCGATAGAGACAAAGATTAACCGGAGGTGACC 208
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/ QY 61 TACTCCAAAGAGGAGGATGGGATTATCAAGAAGCAAGAGATCACTGTTCTATGTAT 120
/ Db 209 TTCTCCAAAGCGCGGAGGCTGCTCAAGAGGCGCAGAGATCTCCGTCCTCTCGCAT 268
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/ QY 121 GCTAAAGTATCTTATCATTTATTTAGTCTTGGGAAGATGTTGAATACTGCAGCCCT 180
/ Db 269 GCCGAGTTCGCGCTATCTGCTTCTCCCAAGGCAAGCTCTACAGTACGCCACCGAC 328
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/ QY 181 TCAACTACGCTGACAGAAATCTTTGGACAA-----ATACCATGGACAATCTGGG 228
/ Db 329 TCCGCGATGACAAAATTTCTGAACGCTATGAGCGATATTCTCTATGCTGAAAGGCTCTT 388
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/ QY 229 AGAAGTGTGGATGCTAGCATGAGAACTCAGCAATGAAGTGAAGTACAGTCAAGAA 288
/ Db 389 ATTTCAGCTGAATCTGAAGTGAAGGAAATGTTGCCACCAATACAGGAACCTGAAGGCC 448
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/ QY 289 GACAATGACAGCATGCAAGTAGAGCTCAGGCATCTGAAGGAGAGGATATCATCATTTG 348
/ Db 449 AAAAAAGAGGCTTCAAGCAACTGAGCAGCAGCTGATAGTCTCATCTGAAGCAGCATCAGA 508
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/ QY 349 ACCATGATAGCTGATGGCTTAGAGGAGCACTTGAAATGGCTTACAGTATCCGG 408
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/ Db 629 CTGCAGGAGGAGAACAAAGGCTTGCAGAGAGGAATTTGCGGAGAGGAGGAGGCGGCTGCGG 688
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/ QY 589 CAGATA 594
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/ Db 749 CAGACA 754
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/ RESULT 11
/ US-08-655-227-7
/ Sequence 7, Application US/08655227
/ Patent No. 6025483
/ GENERAL INFORMATION:
/ APPLICANT: Yanofsky, Martin P.
/ TITLE OF INVENTION: Maize and Cauliflower APETALAI Gene
/ TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Campbell and Flores
/ STREET: 4370 La Jolla Village Drive, Suite 700
/ CITY: San Diego
/ STATE: California
/ COUNTRY: USA
/ ZIP: 92122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/655,227
/ FILING DATE: 05-JUN-1996
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-UD 2143
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1345 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cdna
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 149..968
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 1..1345
/ OTHER INFORMATION: /note= "product = Zea mays AP1."
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/ US-08-655-227-7
/
/ Query Match 10.6%; Score 92; DB 3; Length 1345;
/ Best Local Similarity 48.5%; Pred. No. 1.6e-16;
/ Matches 294; Conservative 0; Mismatches 300; Indels 12; Gaps 1;
/
/ QY 1 ATGGGAGCTGGGAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACAGGAGGTCACC 60
/ Db 149 ATGGGCGCGGAGGTACAGTCAAGCGATAGAGACAAAGATTAACCGGAGGTGACC 208
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/ QY 61 TACTCCAAAGAGGAGGATGGGATTATCAAGAAGCAAGAGATCACTGTTCTATGTAT 120
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/ Db 569 TCAAGGAAGAGCCACCTTATGGCGGAGTCTATTCTTGAGCTACAGAAGAGGAGAGGTCA 628
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/ QY 469 AATAGCGCTCTACTATGAGCTGCAAAACACACAGAGATGAAATATAAGAGATGTG 528
/ Db 629 CTGCAGGAGGAGAACAAAGGCTTGCAGAGAGGAATTTGCGGAGAGGAGGAGGCGGCTGCGG 688
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QY 589 CAGATA 594
Db 749 CAGACA 754

RESULT 12

US-08-655-241-7
; Sequence 7, Application US/08655241
; Patent No. 6025543
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Weigel, Delef
; TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
; TITLE OF INVENTION: Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,241
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: CLASS 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1894
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

FEATURE:
; NAME/KEY: CDS
; LOCATION: 149..968
FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1345
; OTHER INFORMATION: /note= "product = Zea mays AP1."
US-08-655-241-7

Query Match 10.6%; Score 92; DB 3; Length 1345;
Best Local Similarity 48.5%; Pred. No. 1.6e-16;
Matches 294; Conservative 0; Mismatches 300; Indels 12; Gaps 1;

QY 1 ATGGGACCTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAACAGCAGGTGACC 60
Db 149 ATGGGGCGCGGAGGTACAGCTGAGCGGATAGAGAACACAGATATAACCGCAGGTGACC 208
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Db 629 CTGAGGAGGAGACAAAGGCTCTGCAAGAAAGTCTGCGGAGAGGAGGAGGCGCTCGCG 688
QY 529 AGAAACATGGAATGGTATTCATCAGAGGAGCTGGGAACTACAAACACACAGCAG 588
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QY 589 CAGATA 594
Db 749 CAGACA 754

RESULT 13

US-09-149-976-7
; Sequence 7, Application US/09149976
; Patent No. 6127123
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States

Db 209 TTCTCCAGCGCGGAAAGCGCTGCTCAAGAGGCGCAGAGATCTCCGTCCTCTCGCAT 268
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Db 269 GCCGAGTCCCGCTCATCTGCTTTCTCCCCAAGGCGAAGCTCTACGAGTACGCCACCGAC 328
QY 181 TCAACTACGCTGACAGAAATCTTTGGCAA-----ATACCATGGACAATCTGGG 228
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Db 749 CAGACA 754

RESULT 15

US-08-904-284-2
; Sequence 2, Application US/08904284
; Patent No. 6133435
; GENERAL INFORMATION:
; APPLICANT: Fernandez, Donna E.
; APPLICANT: Heck, Gregory R.
; TITLE OF INVENTION: EXPRESSION OF AGL15 SEQUENCE IN
; TITLE OF INVENTION: TRANSGENIC PLANTS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,284
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296.94193
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 795 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-904-284-2

Query Match 10.5%; Score 91; DB 3; Length 795;
Best Local Similarity 66.7%; Pred. No. 2.3e-16;
Matches 130; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 ATGGGACCTGGGAAGGTTTACATCAAGAGGATTCAGAACTCAAGTAAACAGGAGGTGACC 60
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QY 181 TCAACTACGCTGACA 195
Db 181 AGCATGAAGAAAACA 195

Search completed: September 25, 2004, 22:05:11
Job time : 77.5395 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 13:15:32 ; Search time 403.034 Seconds
(without alignments)
9149.204 Million cell updates/sec

Title: US-10-069-527-1

Perfect score: 868

Sequence: 1 atgggacgtgggaaggttga.....aaaaaaaaaaaaaaaaaaaaa 868

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1900s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
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7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	265.2	30.6	947	3	Ad55880 Thalecres
5	259	29.8	780	6	AAC39436 Arabidops
6	259	29.8	783	6	Abk82086 Novel flo
7	258.4	29.8	1065	6	Abk82087 Novel flo
8	257.4	29.7	764	6	Abk82124 DNA encod
9	256.8	29.6	783	6	Abk82088 Novel flo
10	256.8	29.6	789	6	Abk82088 Novel flo
11	256.8	29.6	979	6	Abk82085 DNA encod
12	256.8	29.6	1065	6	Abk82123 DNA encod
13	250	28.8	909	3	Abk82127 Arabidops
14	236.8	27.3	1004	3	AAC3208 Arabidops
15	236	27.2	592	6	AAC4623 Zea mays
16	205.4	23.7	1089	6	Ad42258 Corn AP3
17	148.2	17.1	681	4	Ad42258 Corn AP3
18	148.2	17.1	946	4	AAF85393 Nucleotid
19	148.2	17.1	946	6	Abk85392 Nucleotid
20	148.2	17.1	946	6	Abk88485 Poplar pr
21	147.4	17.0	882	8	ACA62518 Poplar ho
22	146.6	16.9	924	3	AAC51189 Homeotic
23	138.8	16.0	446	3	AAC57943 Poplar fl
					AAC48151 Zea mays

24	136.2	15.7	982	4	AAS00104
25	133.8	15.4	926	6	AAD42259 Soybean A
26	130.4	15.0	1257	6	AAD42257 Corn AP3
27	128.4	14.8	989	3	AAC55879
28	124.2	14.3	959	3	AAC40831 Arabidops
29	122.6	14.1	954	3	AAC51525 Arabidops
30	122.6	14.1	1170	3	AAC51790 Arabidops
31	122	14.1	495	3	AAC48125 Zea mays
32	121.8	14.0	954	3	AAC40685 Arabidops
33	119.4	13.8	121	6	Abk25454 Male-ster
34	119.4	13.8	121	6	Abk25462 Male-ster
35	119.4	13.8	121	6	Abk25466 Male-ster
36	119.4	13.8	121	6	Abk25458 Male-ster
37	119.4	13.8	121	6	Abk25453 Male-ster
38	119.4	13.8	121	6	Abk25465 Male-ster
39	119.4	13.8	121	6	Abk25461 Male-ster
40	119.4	13.8	121	6	Abk25457 Male-ster
41	112	12.9	386	3	AAC57268 Eucalyptu
42	109.8	12.6	613	3	AAC57279 Eucalyptu
43	109	12.6	909	3	AAF9364 Plant Fra
44	109	12.6	4285	4	AAF85391 Nucleotid
45	109	12.6	4285	6	Abk88484 Poplar pr

ALIGNMENTS

RESULT 1
AAS00103
ID AAS00103 standard; cDNA; 868 BP.
XX AAS00103;
AC AAS00103;
XX
DT 11-SEP-2003 (revised)
DT 17-MAY-2001 (first entry)
XX
DE Granny Smith apple cDNA encoding MdPI.
XX
KW Granny Smith apple; MdPI; seedless fruit; horticulture;
KW accelerated breeding programme; cross pollination; transgenic plant;
KW biennial bearing tendency; codling moth; ss.
XX
OS Malus x domestica; var. Granny Smith.
XX
FH Key Location/Qualifiers
CDS
FT
FT /tag= a
FT /product= "MdPI"
FT primer_bind 1..15
FT /tag= b
FT /label= PCR_primer_P1_binding_site 19..41
FT primer_bind /tag= c
FT /label= PCR_primer_P5_binding_site 291..312
FT primer_bind /tag= d
FT /label= PCR_primer_P3_binding_site 314..334
FT primer_bind /tag= e
FT /label= PCR_primer_P4_binding_site complement(609..626)
FT primer_bind /tag= f
FT /label= PCR_primer_P2_binding_site complement(770..791)
FT primer_bind /tag= g
FT /label= PCR_primer_P7_binding_site complement(818..840)
FT primer_bind /tag= h
FT /label= PCR_primer_P6_binding_site
XX WC200117334-A1.
PN
XX
XX WC200117334-A1.
PD 15-MAR-2001.

XX 07-SEP-2000; 2000WO-NZ000176.
 XX 07-SEP-1999; 99NZ-00337688.
 XX (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.
 XX Yao J, Morris BA;
 XX WPI; 2001-235145/24.
 XX P-PSDB; RAU00186.
 XX New genetically modified fruiting plants that does not functionally
 XX express MdPI or MdAP3 peptides, useful for producing seedless fruits,
 XX specifically apple and its related species.
 XX Claim 10; Fig 2; 4ipp; English.
 XX The sequence encodes Granny Smith apple MdPI. The invention concerns a
 XX fruiting plant that has been genetically modified so that it does not
 XX functionally express the MdPI or MdAP3 peptide, producing seedless
 XX fruits. The DNA constructs encoding non-functional variants of MdPI/MdAP3
 XX may be used to transform fruiting plants, specifically apple and pear.
 XX The polynucleotides may be used in modulating, reducing or eliminating
 XX seed-bearing capacity in fruiting plants, used in horticulture, and in
 XX breeding programmes to monitor the progress in breeding a stable seedless
 XX fruiting plant. The polynucleotides may also be used in programmes for
 XX identifying nucleic acid variants from fruiting plants. They can be used
 XX for pre-selecting plants (mutated in MdPI, MdAP3 or their equivalents),
 XX for use in an accelerated breeding programme to produce seedless fruit.
 XX They may also be used in designing probes and primers for MdPI or MdAP3,
 XX or their variants. The seedless fruiting plant is more convenient than
 XX seeded fruit since these can be cropped without pollination, reducing
 XX dependence on bees, pollinator varieties and warm weather at flowering.
 XX The absence of pollen is also advantageous to alleviate environmental
 XX concerns regarding the transfer of transgenes to non-transgenics by cross
 XX pollination. Seedless cultivars can also avoid or reduce biennial bearing
 XX tendencies that have been attributed to the inhibition of flower bud
 XX formation by developing seeds and are less susceptible to codling moth
 XX compared to seeded fruit. (Updated on 11-SEP-2003 to standardise OS
 XX field)
 XX SQ Sequence 868 BP; 296 A; 152 C; 208 G; 212 T; 0 U; 0 Other;
 Query Match 100.0%; Score 868; DB 4; Length 868;
 Best Local Similarity 100.0%; Pred. No. 3.2e-210;
 Matches 868; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGGACGTGGGAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACAGGAGGTGACC 60
 Db |||||
 QY 1 ATGGGACGTGGGAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACAGGAGGTGACC 60
 Db |||||
 QY 61 TACTCCAGAGGAGGAGTGGATTATCAAGAGGCAAGAGGATCACTGTTCTATGTGAT 120
 Db |||||
 QY 61 TACTCCAGAGGAGGAGTGGATTATCAAGAGGCAAGAGGATCACTGTTCTATGTGAT 120
 Db |||||
 QY 121 GCTAAAGTATCTTTATCATTTTATCTAGCTCTGGGAAGATGGTTGAATPACGAGCCCT 180
 Db |||||
 QY 121 GCTAAAGTATCTTTATCATTTTATCTAGCTCTGGGAAGATGGTTGAATPACGAGCCCT 180
 Db |||||
 QY 181 TCAACTACGCTGACAGAACTCTGGCAATACCAATGGCAATCTGGGAGAGGTTGG 240
 Db |||||
 QY 181 TCAACTACGCTGACAGAACTCTGGCAATACCAATGGCAATCTGGGAGAGGTTGG 240
 Db |||||
 QY 241 GATGCTAAGCATGAGAACTCTGAGCAATCAAGTGGATAGAGTCAAGAAAGACAATGACAGC 300
 Db |||||
 QY 241 GATGCTAAGCATGAGAACTCTGAGCAATCAAGTGGATAGAGTCAAGAAAGACAATGACAGC 300
 Db |||||
 QY 301 ATGCAAGTACGCTCAGGATCTGAGGAGGAGGATATCACATCAATGCAATGATAGAG 360
 Db |||||
 QY 301 ATGCAAGTACGCTCAGGATCTGAGGAGGAGGATATCACATCAATGCAATGATAGAG 360
 Db |||||
 QY 361 CTGATGGCCTTAGAGGAAGCACTTGAAATATGGCCTTACAAAGTATCCGGGCAACAGCAGTCC 420
 Db |||||

Db ||||| CTGATGGCCTTAGAGGAAGCACTTGAAATATGGCCTTACAAAGTATCCGGGCAACAGCAGTCC 420
 QY ||||| 421 AAGTTCCGTGCACATGATGAGAGACAATGGAAAGCACTGGAAAGATGAGAATAAGCGGCTC 480
 Db ||||| 421 AAGTTCCGTGCACATGATGAGAGACAATGGAAAGCACTGGAAAGATGAGAATAAGCGGCTC 480
 QY ||||| 481 ACTTATGAGCTGCAGAAACCAACAGGAGATGAAAAATAAAGAGAAATGTCAGAAACATGGA 540
 Db ||||| 481 ACTTATGAGCTGCAGAAACCAACAGGAGATGAAAAATAAAGAGAAATGTCAGAAACATGGA 540
 QY ||||| 541 AATGGGTATCATCAGAGGAGCTGGGAACTACAAACCAACAGGAGGAGATACCTTTT 600
 Db ||||| 541 AATGGGTATCATCAGAGGAGCTGGGAACTACAAACCAACAGGAGGAGATACCTTTT 600
 QY ||||| 601 GCCTTCCCGTGCAGGCTTATTCAGCAAAATCTCCAGGAGAGAAATCTAATAGATATATCT 660
 Db ||||| 601 GCCTTCCCGTGCAGGCTTATTCAGCAAAATCTCCAGGAGAGAAATCTAATAGATATATCT 660
 QY ||||| 661 TGCATTTCATGCTCTTTCTTAACCTAGTTATATATCTTCCACCTCTCTCTCTCTTTTCA 720
 Db ||||| 661 TGCATTTCATGCTCTTTCTTAACCTAGTTATATATCTTCCACCTCTCTCTCTCTTTTCA 720
 QY ||||| 721 TCTGTCAAGGAGTCTTAAAGTTTATGTCAGATTTCCAAATGGTTGTAATGGAATAGCTT 780
 Db ||||| 721 TCTGTCAAGGAGTCTTAAAGTTTATGTCAGATTTCCAAATGGTTGTAATGGAATAGCTT 780
 QY ||||| 781 CGTTATGAGGCTTTGTTGTGAACCTTCTAATAATTAAGGCGTGCATGAACCTCGTTTGTG 840
 Db ||||| 781 CGTTATGAGGCTTTGTTGTGAACCTTCTAATAATTAAGGCGTGCATGAACCTCGTTTGTG 840
 QY ||||| 841 GGRAAAAAAAAAAAAAAAAAAAAAA 868
 Db ||||| 841 GGAIAAAAAAAAAAAAAAAAAAAAAA 868
 XX RESULT 2
 XX AAQ55089
 XX ID AAQ55089 standard; cDNA; 780 BP.
 XX AC AAQ55089;
 XX XX
 XX 16-OCT-2003 (revised)
 XX 25-MAR-2003 (revised)
 XX 25-JUN-1994 (first entry)
 XX DE fbpl cDNA for reverse genetic techniques.
 XX KW Flower; morphology; petals; MADS box protein; toxin gene; insect;
 XX resistance; Frankliniella occidentals; plant; ss.
 XX OS Petunia x hybrida.
 XX FH Key Location/Qualifiers
 XX primer_bind 8..22
 XX FT /*tag= a
 XX FT /note= "PCR primer"
 XX FT 731..753
 XX FT /*tag= b
 XX FT /note= "PCR primer"
 XX XX
 XX EN W09400582-A2.
 XX XX
 XX PD 06-JAN-1994.
 XX XX
 XX PF 07-JUN-1993; 93WO-NL000121.
 XX XX
 XX PR 30-JUN-1992; 92EP-00201951.
 XX XX
 XX FA (CPRO-) CPRO-DLO CENT PLANT BREEDING & REPRODUCT.
 XX XX
 XX PI Van Tunen AJ, Mollema C, Angenent GC, Dons JUM;
 XX XX

DR WPI; 1994-026218/03.
XX P-PSDB; AAR46555.
PT New nucleic acid which alters flower morphology - by suppressing petals
PT and stamen(s), or converts them to other organs, partic. to produce
PT transgenic plants less susceptible to insect pests.
XX
PS Disclosure; Fig 1A; 33pp; English.
XX
XX A flower specific gene fbpl was isolated from the genome of Petunia
CC hybrida. This gene has the features of a transcription factor and belongs
CC to the group of MADS box genes. The fbpl gene is only active during
CC differentiation of floral organ primordia and plays a crucial role in the
CC determination of part of the floral meristem into petals and stamen
CC primordia. Plants transformed with the gene are less attractive to insect
CC pests so have better resistance to them; specifically cucumber plants are
CC protected against Frankliniella occidentalis but the method can be used
CC for other, esp. parthenocarpic and/or apomictic plants. The plants are
CC also less susceptible to secondary fungal infection. Elimination of
CC petals may improve photosynthesis and seed yield may be increased. See
CC also AAQ5590-3. (Updated on 05-MAR-2003 to correct PN field.) (Updated
CC on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 780 BP; 277 A; 120 C; 172 G; 211 T; 0 U; 0 Other;
Query Match 33.6%; Score 291.4; DB 2; Length 780;
Best Local Similarity 67.8%; Pred. No. 7.5e-64;
Matches 444; Conservative 0; Mismatches 196; Indels 15; Gaps 2;
QY 1 ATGGGAGCTGGGAGGTTGAGATCAAGAGGATTGAGAACTCAAGTCAACGCGGAGGTGACC 60
DB 8 ATGGGAGAGGAAAGATAGAGATAAAGAAATAGAAACTCAAGCAACGACAGCAAGTAAT 67
QY 61 TACTCAGAGGAGGAGGAGTGGATATCAAGAGGCAAGGAGATCACTGTTCTATCTGAT 120
DB 68 TACTCAAAAAGAGAAATGGGATCTTGAAAAAGCTTAAGGAAATAGTGTCTTTGTGAT 127
QY 121 GCTAAAGTATCTCTTATCAATTTCTAGCTCTGGGAGAGTGTGTAATCTACGCCCTT 180
DB 128 GCTCGTGTCTCTGTTATCAATTTTGTAGCTCTGGCAAGATGATGATCTCT-----CT 181
QY 181 TCAACTACGCTGACAGAAATCTTGGAACAATACCATGGACAATCTGGGAAGAAGTTGTGG 240
DB 182 TCTACTTCTGTTGTTGATTTTGGATCAATATATCAAGGCTTACTGTGTAAGATTGTTG 241
QY 241 GATCTAAGCATGAGACCTCAGCAATGAAGTGGATAGTCAAGAAAGCAATGACAGC 300
DB 242 GATCTAAGCATGAGAACTTGGACAATGAATCAACAAGTCAAGAAAGCAATGACAC 301
QY 301 ATGCAAGTAGAGCTCAGGCATCTGAAGGAGAGGATATCATCAATTAACCATGTAGAG 360
DB 302 ATGCAAAATTGAATCAGGCACCTTGAAGGGTGAAGATATCATCTTTGAACCATAGAG 361
QY 361 CTGATGCCCTTAGAGGAGCACTTGAATGGCCTTACAGTATCCGGGACAGCAGTCC 420
DB 362 CTCATGATATTGGAAGATGCCCTTGAATGGACTCACTAGTATTCGTAAACAACAGAT 421
QY 421 AAGTTCTGTCGACATGATGAGAGACAAATGGAAGGCACTGGAAGATGAGAATAAGCGCTC 480
DB 422 GAGTCTCTGAGATGATGAGAAAGAAAGACTCAAGTATGGAGGAGGAGCAAGCACTT 481
QY 481 ACTTATGAGCTGCAAAAACAACAGAGATGAATAAAGAGATGTGAGAAACATGGAA 540
DB 482 AATTGCCAATTCGCCCACTTGAGATAGCAACCATGAATAGGAATATGGGAGAAATGGC 541
QY 541 AATGGTATCATCAGAGCAGCTGGGAACTFACAAACACACACAGCAGCAGATACCTTTT 600
DB 542 GAAGTGTTCAGCAGAGGAG-----AATCATGCTACCAAAACCATATGCCCTTTT 592
QY 601 GCCTTCCGCTGCGACCTTATTCAGCAAAATCTCCAGGAGAGAAATCTTAATAGATA 655
DB 593 GCCTTCCGAGTACAAACCAATGACGCAAAATTTGAGGAGAGGTTGTAAAAAAAGA 647

RESULT 3
ADD55880
ID ADD55880 standard; cDNA; 896 BP.
XX
AC ADD55880;
XX
DT 15-JAN-2004 (first entry)
DE Thalecress environmental stress-related cDNA #127.
XX
KW Thalecress; environmental stress; ss; plant; viral infection;
KW fungal infection; microbial infection; herbicide resistance; heat; cold;
KW heavy metal; low light; drought; osmotic stress; salt concentration;
KW transgenic.
XX
OS Arabidopsis thaliana.
XX
PN US2003131386-A1.
XX
PD 10-JUL-2003.
XX
PF 22-OCT-2002; 2002US-00278536.
XX
PR 23-MAR-1999; 99US-0125814P.
PR 22-MAR-2000; 2000US-00532591.
XX
XX (SANA/) SAMAHA R.
PA (HEAR/) HEARD J.
PA (JIAN/) JIANG C.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER L.
PA (RIEC/) RIECHMANN J L.
PA (YUGG/) YU G.
PA (KEDD/) KEDDIE J.
PA (RATC/) RATCLIFFE O.
PA (PILG/) PILGRIM M.
PA (ADAM/) ADAM L.
PA (BROU/) BROUN P.
PA (ZHAN/) ZHANG J.
XX
PI Samaha R, Heard J, Jiang C, Pineda O, Reuber L, Riechmann JL;
PI Yu G, Keddie J, Ratcliffe O, Pilgrim M, Adam L, Broun P, Zhang J;
XX
DR WPI; 2003-829608/77.
XX
XX New recombinant polynucleotide for altering the regulation of gene
PT expression of plants to modify the plant's traits, particularly the
PT plant's environmental stress tolerance.
XX
PS Claim 14; SEQ ID NO 238; 219pp; English.
XX
CC The invention relates to a recombinant polynucleotide that alters a
CC plant's environmental stress tolerance when compared with the same trait
CC of another plant lacking the recombinant polynucleotide. Also included
CC are a transgenic plant comprising the novel recombinant polynucleotide
CC having a sequence that encodes a polypeptide comprising at least 6
CC consecutive amino acids of any of the 55 250-500 residue amino acid
CC sequences (s1), given in the specification, altering the environmental
CC stress response or tolerance of a plant, or altering a plant's trait and
CC altering the expression levels of at least one gene in a plant. The
CC recombinant polynucleotide and methods are useful for altering the
CC regulation of gene expression of plants to modify the plant's traits, in
CC particular with respect to environmental stress responses (e.g. to viral
CC infection, fungal infection, microbial infection, herbicide resistance,
CC heat, cold, heavy metals, low light, drought, osmotic stress and salt
CC concentration). The present sequence is an environmental stress related
CC polynucleotide of the invention.
XX
SQ Sequence 896 BP; 285 A; 143 C; 218 G; 250 T; 0 U; 0 Other;

Query Match 30.6%; Score 265.2; DB 9; Length 896;
Best Local Similarity 68.0%; Pred. No. 3.6e-57;

ABK82086
 ID ABK82086 standard; cDNA; 780 BP.
 XX
 AC ABK82086;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 XX Novel floral meristem identity gene LpMADS1 contig #1.
 DE
 DE Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein; ss.
 XX
 OS Lolium perenne.
 XX
 FN WO200233091-A1.
 XX
 XX 25-APR-2002.
 PD
 XX 17-OCT-2001; 2001WO-AU001311.
 XX
 XX 19-OCT-2000; 2000AU-00000873.
 XX
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 XX
 PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX
 XX WPI; 2002-454601/48.
 DR
 XX New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 XX
 XX Claim 3; Fig 29; 290pp; English.
 FS
 XX The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence represents a contig
 CC polynucleotide novel floral meristem identity protein involved in floral
 CC development and a potential target for manipulating plant life cycles

SQ Sequence 780 BP; 229 A; 203 C; 206 G; 136 T; 0 U; 6 Other;
 Query Match 29.8%; Score 259; DB 6; Length 780;
 Best Local Similarity 64.5%; Pred. No. 1.3e-55;
 Matches 426; Conservative 0; Mismatches 216; Indels 18; Gaps 2;
 QY 1 ATGGGACGTGGGAGTTGAGATCAGAGAGATTGAGAACTCAAGTAACAGCAGGTGACC 60
 DB |||||
 QY 84 ATGGGCGGTGGGAAGATCGAGATCAAGAGAGATCGAGAACCGCAGGTGACC 143
 DB |||||
 QY 61 TACTCCAAGAGAGAGAAATGGGATATTCAAGAGGCAAGAGAGATCACTGTCTTATGTGAT 120
 DB |||||
 QY 144 TTCTCCAAGCGCAAGACGGGATCTCTCAAGAGGCGCAAGAGATCAGCGTCTCTGGCAG 203
 DB |||||
 QY 121 GCTAAAGTATCTCTTATCATTTATCTAGCTCTGGAGAGATGGTGTGAATCTGAGCGCTT 180
 DB |||||
 QY 204 GCCGAGGTGGGCTGCTGCTCTTCTCCAGCGCGGCAAGCTCTACGACTTCTGCTCCCA 263
 DB |||||
 QY 181 TCAACTAGCTGACAGAAATCTTGACAAATACCATGGACAACTCTGGGAAGAGTTGTGG 240
 DB |||||
 QY 264 AAGACATCGCTATCAAGATCTTGGAGAGATCCAGACCACTCCGGAGAGATCTGTGG 323
 DB |||||
 QY 241 GATGCTAAGCATGAGAACCTCAGCAATGAAGTGGATAGAGTCAAGAAAGACAATGACAGC 300
 DB |||||
 QY 324 GATGAGAAACACAAGAGCCTCAGTGGGAGATTGATCGAATCAAGAAAGAAAATGACAAC 383
 DB |||||
 QY 301 ATGCAAGTAGAGCTCAGGCATCTGAAGGGAGAGAGATATCATCATTTGAACCATGTAGAG 360
 DB |||||
 QY 384 ATGCAGATCGAGCTCAGGCATCTGAAAGGCGAAGATCTGAACTCCTGCAACCCCAAGAG 443
 DB |||||
 QY 361 CTGATGGCTTTAGAGGAAGCACTTGAATAATGGCCCTTACAAGTATCCGGGACAAGCAGTCC 420
 DB |||||
 QY 444 TTGATCATGATTGAGGAAGCACTTGAATATGACTGACAGCGCTGCATGAAAACAGATG 503
 DB |||||
 QY 421 AAGTTCGTGCATGATGAGAGACAATGGAAGGCATCTGGAAGATGAGATTAAGCGCTC 480
 DB |||||
 QY 504 GAGCAGTACGACAGCGCTGATGAAACCTGGCAAGATGCTAGAAGATGAGAACAAAGTTGCTC 563
 DB |||||
 QY 481 ACTTATGAGCTGCAAAACCAACAGGAGATGAAATAAAGAGATGTGAGAAACATGAA 540
 DB |||||
 QY 564 GCATCTAAACTGC---ATCAGCAGATATTGCGCTGACGGGACATGAGGGAGCTTGAG 620
 DB |||||
 QY 541 AATGGTATCATCAGAGCAGCTGGGAACTACAAACAAACAGCAGCAGATACCTTTT 600
 DB |||||
 QY 621 CTGCTTACCATCCG-----GACAGGAGACTTTGCGAGCCAGATGCCGATC 665
 DB |||||
 QY 601 GCCTTCGCGTGCAGCCTTATTCAGCCAAATCTCCAGGAGAGAAATCTAATTAGATATATCT 660
 DB |||||
 QY 666 ACGTTCGCGTGCAGCCTTAGCCACCCCACTGCGAGGAGACAGCTAGGCGCGNTTATCT 725
 DB |||||

RESULT 6

ABK82087

ID ABK82087 standard; cDNA; 783 BP.

XX

AC ABK82087;

XX

DT 27-AUG-2002 (first entry)

XX

XX Novel floral meristem identity gene LpMADS1 contig #2.

XX

XX Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;

KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;

KW HB-like protein; plant growth; plant architecture;

KW inflorescence development; flower development; embryo development;

KW seed development; flower organ identity; phase change; male sterility;

KW hybrid seed production; herbage quality; early maturing crop;

KW biomass increase; branching increase; blocking flowering;

KW allergenic pollen; floral meristem identity protein; ss.

XX

OS Lolium perenne.

XX

XX WO200233091-A1.

FN

XX PD 25-APR-2002.
 XX PF 17-OCT-2001; 2001WO-AU001311.
 XX PR 19-OCT-2000; 2000AU-00000873.
 XX PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 XX PA (AGRE-) AGRESEARCH LTD.
 XX PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX DR WPI; 2002-454601/48.
 XX
 XX New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 XX
 XX Claim 3; Fig 29; 290pp; English.
 XX
 CC The invention describes a substantially purified or isolated polypeptide
 CC (i) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (ii) encoding (i), a construct (iii) comprising (ii), or a
 CC vector (iv) comprising (ii), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (ii), (iii) or (iv) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another. Leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence represents a contig
 CC polynucleotide novel floral meristem identity protein involved in floral
 CC development and a potential target for manipulating plant life cycles
 XX
 SQ Sequence 783 BP; 233 A; 204 C; 208 G; 136 T; 0 U; 2 Other;

Query Match 29.8%; Score 259; DB 6; Length 783;
 Best Local Similarity 64.5%; Pred. No. 1.3e-55;
 Matches 426; Conservative 0; Mismatches 216; Indels 18; Gaps 2;

QY 1 ATGGAGCTGGGAGGTTGAGATCAAGAGGATTCAGAACTCAAGTACAGCGAGGTGACC 60
 DB 82 ATGGGGCTGGGAGATCGAGATCAAGAGATCGAGAACAGACACCCAGGTGACC 141
 QY 61 TACTCCAGAGGAGGATTCAGAGGATTCAGAGGAGGAGGATTCAGTTCATGTGAT 120
 DB 142 TTCTCCAGCGCAAGACGGGATCTCTCAAGAGGCGCAAGGAGATCAGCGTCTCTGGAC 201
 QY 121 GCTAAAGTATCTTATCATTTATCTAGCTCTGGAGATGGTTGAATCTACGACCT 180
 DB 202 GCCAGGTGCGGTGCTGCTTCTCCAGCGCGGCAAGTCTAGAGACTTCTGTCCTCCCA 261
 QY 181 TCAACTAGCTGACAGAAATCTTGGACAAATPACCATGGAATCTGGGAAGAAGTTGTGG 240
 DB 262 AAGACATCGCTATCAAGATCTTGGAGAGGTACCAGACCAACTCCGGGAAGATCTGTGG 321

QY 241 GATGCTAAGCATGACAACTCAGCAATGAAGTGGTAGAGTCAAGAAAGACAATGACAGC 300
 DB 322 GATGAGAAACACAGAGGCTCAGTCGGGAGATTGATCGAATCAAGAAAGAAATGACAAC 381
 QY 301 ATGCAAGTAGAGCTCAGGCACTCTGAAGGAGAGGATATCACATCTATTGAACCATGTAGAG 360
 DB 382 ATGCAGATCGAGCTCAGGCACTTGAAGGCGGAAGATCTGAACTCACTGCAACCCAAAGAG 441
 QY 361 CTGATGGCTTAGAGGAAGCACTTGAAATAGCCCTTACAAGTATCCGGGACAAGCAGTCC 420
 DB 442 TTGATCATGATTGAGGAAGCACTTGATATGGACTGACAGGCTGCTGATGAAAAACAGATG 501
 QY 421 AAGTTCGTGATGATGAGAGACAAATGGAAGGCACTTGAAGATGAGATGAGAAAGCCCTC 480
 DB 502 GAGCACTAGCAGAGCTGATGAAACTGCGCAAGATGCTAGAGATGAGAAACAAGTTGTCT 561
 QY 481 ACTTATGAGCTCAAAAACACAGAGATGAAAATAAAAGAGAAATGTGAGAAACATGGA 540
 DB 562 GCATCTAACTGC---ATCAGCAAGATATTGGCTGAACGGGAACATGAGGAGCTTGAG 618
 QY 541 AATGGGTATCATCAGAGGAGCTGGGAACTATCAACAACAACAGCAGCAGATACCTTTT 600
 DB 619 CTTGGTTACCATCCG-----GACAGGGACTTTTGCAGCCAGATGCCGATC 663
 QY 601 GCCTTCCGGCTGAGCCTATTTCAGCCAAATCTCCAGGAGAGAACTCTAATTAGATATATCT 660
 DB 664 ACCTTCCGGCTGAGCCTAGCCACCCCACTGAGGAGAGACAGTAGGCGGNTTAATCT 723
 RESULT 7
 ABK82124
 ID ABK82124 standard; cDNA; 1065 BP.
 XX
 AC ABK82124;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE DNA encoding novel floral meristem identity protein LpMADS1b.
 XX
 KW Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein; gene; ss.
 XX
 OS Lolium perenne.
 OS
 PN WO200233091-A1.
 XX
 PD 25-APR-2002.
 XX
 PF 17-OCT-2001; 2001WO-AU001311.
 XX
 PR 19-OCT-2000; 2000AU-00000873.
 XX
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 XX
 PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX
 DR WPI; 2002-454601/48.
 DR P-PSDB; ABG60942.
 XX
 PT New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 XX
 PS Claim 3; Fig 59; 290pp; English.

XX CC The invention describes a substantially purified or isolated polypeptide
CC (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
CC MADS-box (MADS), MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
CC proteins, AP2A2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
CC and HB-like proteins, or their functionally active fragments or variants.
CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
CC vector (IV) comprising (II), is useful for modifying plant life cycles
CC and/or growth phases, flowering processes, flowering and/or plant
CC architecture and/or flower and/or inflorescence development in a plant,
CC which involves introducing (II), (III) or (IV) into the plant. The
CC individual or simultaneous enhancement or downregulation of MADS-box gene
CC activities may alter flower, embryo and seed development, e.g., enhance
CC or inhibit embryo differentiation and growth or alter flower organ
CC identity through conversion of one floral organ in another. Manipulation
CC of CEN or HB activity in plants alters the control of phase change,
CC flowering time and the number of leaves made before flowering.
CC Manipulation of AP2 activity in plants alters flower organ identity
CC through conversion of one floral organ in another, leads to a change in
CC the number of floral organs and flowering architecture. Manipulation of
CC flowering plant architecture has a wide range of applications such as:
CC inducing male sterility for hybrid seed production; changing flower
CC architecture for enhancing value of ornamentals; delaying flowering in
CC forage grasses thus stopping the formation of less digestible stems and
CC increasing herbage quality; altering flowering time allowing early
CC maturing crops; delaying vegetative phase to increase biomass production;
CC increasing branching to enhanced business in fruit trees; altering plant
CC size e.g. shorter plant stature; and in blocking flowering and reducing
CC release for allergenic pollen. This sequence encodes a novel floral
CC meristem identity protein involved in floral development and a potential
CC target for manipulating plant life cycles

Sequence 1065 BP; 328 A; 253 C; 267 G; 217 T; 0 U; 0 Other;

Query Match	29.8%;	Score 258.4;	DB 6;	Length 1065;
Best Local Similarity	64.5%;	Pred. No. 2e-55;		
Matches 426;	Conservative 0;	Mismatches 216;	Indels 18;	Gaps 2
QY	1	ATGGGACGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACAGGACAGGTGACC	60	
Db	128	ATGGGGCGTGGGAAGATCGAGATCAAGAGGATCGAGAACAGAGCAACCGCCAGGTGACC	187	
QY	61	TACTTCAAGAGGAGGATGGGANTTATCAAGAGGCCAAGGAGATCACTGTTCTTGTGTGAT	120	
Db	188	TCTTCCAAAGCCAAAGACGGGATCCTCAAGAAGGCCAAGGAGATCAGCTGTCTTCGGAC	247	
QY	121	GCTAAGATGATCTCTTATCATTTATTCTAGCTCTCTGGGAAGATGTTGAATCTGCAGCCCT	180	
Db	248	GCCGAGGTCGGCGTCTCTTCTCCAGCGCCGGCAAGCTCTACGACTTCTGCTCCCCA	307	
QY	181	TCAACTACGCTGCACAGAAATCTTGGACAANAATCAATGAGCAATCTCTGGGAAGAAGTTGTGG	240	
Db	308	AAGACATCGCTATCAAGAATCTTGGAGAAGTACCAAGCAACTCCGGGAAGATATCTGTGG	367	
QY	241	GATGCTAAGCATGAGAACTCAGCAATGAAAGTGGATAGAGTCAAGAAAGACAAATGACAGC	300	
Db	368	GATGAGAAACAAGAGGCCTCAGTGCAGGATTTGATCGAATCAAGAAAGAAATGACAAC	427	
QY	301	ATGCAAGTAGAGCTCAGGCATCTGAAGGGAGAGGATATCACATCATTTGAACATGTAGAG	360	
Db	428	ATGCAGATTCGAGCTCAGGCATCTGAAGGGGGAAGACTGAACCTCATCTGCACCCCAAGAG	487	
QY	361	CTGATGGCCCTTAGAGGAAGCACITTTGAAAATGGCCCTTACAAGTATCCGGGACAAGCAGTCC	420	
Db	488	TTGATCATGATTTAGGAAGACATTTGATAATGGACTGACAGCCCTGCATGAAAAACAGATG	547	
QY	421	AAGTTCGTGCACATGATGAGAGACAATGGAAAGGCCATCGAAGATCAGAAATGAAGCCCTC	480	
Db	548	GAGCNACTACGACAGCTGATGMAAACTTGGCAGATGCTTAGAGATGAGAACCAAGTTGCTC	607	
QY	481	ACTTATGAGCTGCAAAAACAACAGGAGATGAAAATAAAAAGAGAAATGTGAGAAACATGAA	540	
Db	608	GCATCTAAACTGC---ATCAGCAAGATATTGCCTGAAACGGGAACATGAGGAGCTTCAG	664	

CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence represents a contig
 CC polynucleotide novel floral meristem identity protein involved in floral
 CC development and a potential target for manipulating plant life cycles
 XX
 SQ Sequence 764 BP; 225 A; 202 C; 206 G; 129 T; 0 U; 2 Other;

Query Match 29.7%; Score 257.4; DB 6; Length 764;
 Best Local Similarity 64.4%; Pred. No. 3.2e-55;
 Matches 425; Conservative 0; Mismatches 217; Indels 18; Gaps 2;

QY 1 ATGGGACGTGGGAAGTGTGATCAAGAGATTGAGAACTCAAGTCAAGCGCAGGTGACC 60
 DB 84 ATGGGCGCGGGAAGATCGAGATCAAGAGATCGAGAACCCAGAGCAACGCCAGGTGACC 143
 QY 61 TACTCCAGAGGAGGATGGATTATCAAGAGGCAAGAGAGATCACTGTCTTCTATGTGAT 120
 DB 144 TTCTCCAGCGCAGAGACGGGATCTCTCAAGAGGCCAGAGAGATCGGTCTCTCGAC 203
 QY 121 GCTAAAGTATCTCTTATCATTTATTTCTGCTTGGGAAGATGGTTGAATCTACGCCCT 180
 DB 204 GCGAGGTGCGGCTGCTGCTCTCCAGCGCGCAAGCTCTACGACTTCTCTCTCCCC 263
 QY 181 TCAACTACGTGACAGAAATCTTGGCAAAATACATGGCAATCTGGGAGAGTGTGG 240
 DB 264 AAGACATCGGTATCAAGAACTTGGGAGAGTACAGACCACTCCGGGAGATGACTGTGG 323
 QY 241 GATGCTAAGCATGAGAACTCTCAGCAATGAAGTGTGATAGATCAAGAAAGCAATGACAGC 300
 DB 324 GATGAGAAACACAGAGCCTCAGCGGAGATTGATCGAATCAAGAAAGAAATGATAAC 383
 QY 301 ATGCAAGTACAGCTCAGCGATCTCAAGGGAGAGGATATCATCATTTGAACCATGTAGAG 360
 DB 384 ATGCAGATCAGCTCAGCGACTTGAAGGGGAGATCTGAACCTCACTGCAACCCAAAGAG 443
 QY 361 CTGATGCGCTTAGAGGAGCACTTGAATAATGGCTTACAAGTATCCGGGCAAGCAGTCC 420
 DB 444 TTGATCATGATTGAGGAGCACTTGATATGAGTACAGCGCTGATGAAACACAGATG 503
 QY 421 AAGTCTCTGCATGATGAGAGCAATGGAAGGCACTGGAAGATGAGATAAGCGCCTC 480
 DB 504 GAGCACTACGACAGGCTGATGAAACTGCGCAAGATGCTAGAAGATGAGAAAGTGTCTC 563
 QY 481 ACTATCAGCTGCAAAACACAGGAGATGAAATTAAGAGATGTGAGAAACATGGAA 540
 DB 564 GCATTTAACTGC---ATCAGCAAGATATTGGCTGAACGGGAACATGAGGGAGCTTGAG 620
 QY 541 AATGGGTATCATCAGAGCGAGCTGGGAACTACAACCAACACAGCAGCAGATACCTTTT 600
 DB 621 CTTCGTTACCATCG-----GACAGGCACTTTGAGCCAGATGCCGATC 665
 QY 601 GCCTTCGCGTGCAGCTATTCACCAAAATCTCCAGAGAGATCTAATTAGATATATCT 660
 DB 666 ACGTTCGCGTGCAGCTAGCCACCAACCTCGCAGGAGAACAGCTAGGCCGNTTAATCT 725

RESULT 9

ABK82088

ID ABR82088 standard; cDNA; 783 BP.

XX AC ABR82088;

XX DT 27-AUG-2002 (first entry)

XX DE Novel floral meristem identity gene LpVADS1 contig #3.

XX KW Ryegrass; fescue; VADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;

KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein; ss.
 XX Lolium perenne.
 OS
 XX WO200233091-A1.
 FN
 XX 25-APR-2002.
 XX 17-OCT-2001; 2001WO-AU001311.
 XX 19-OCT-2000; 2000AU-00000873.
 XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRSEARCH LTD.
 XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX WPI; 2002-454601/48.
 XX
 XX New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 XX
 XX Claim 3; Fig 29; 290pp; English.
 PS
 XX The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or down-regulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence represents a contig
 CC polynucleotide novel floral meristem identity protein involved in floral
 CC development and a potential target for manipulating plant life cycles
 XX
 SQ Sequence 783 BP; 232 A; 204 C; 208 G; 138 T; 0 U; 1 Other;

Query Match 29.6%; Score 256.8; DB 6; Length 783;
 Best Local Similarity 64.4%; Pred. No. 4.6e-55;
 Matches 425; Conservative 0; Mismatches 217; Indels 18; Gaps 2;

QY 1 ATGGGACGTGGGAAGTGTGAGATCAAGAGGATGTGAACTCAAGTCAAGCGCAGGTGACC 60
 DB 78 ATGGGCGCGGGAAGATCGAGATCAAGAGATCGAGAACCCAGAGCAACGCCAGGTGACC 137

QY 61 TACTCCAGAGGAGGATGGATTATCAAGAGGCAAGAGATCACTGTTCTATGTAT 120
 Db 138 TTCTCCAGCGCAAGACCGGATCTCAAGAGGCCAAGAGATCAGCGTGTCTCGGAC 197
 QY 121 GCTAAAGTATCTTATCATTTATCTAGCTCTGGGAGATGTTGAATACTGACGCT 180
 Db 198 GCCAGATCGCGTGTCTGCTTCTCCAGCGCGGAGATCTTACGACTTCTGCTCCCC 257
 QY 181 TCAACTACGCTGACAGAAATCTTGGCAAAATACCATGCGCAATCTCGGAGAGTTGTGG 240
 Db 258 AAGACATCGCTATCAAGATCTTGGAGAGTACCAGACCAACTCCGGAGATCTGTGG 317
 QY 241 GATGCTAAGCATGAGACCTCAGCATGAGTGAAGTGAAGTCAAGAAAGACATGACAG 300
 Db 318 GATGAGAAACACAGAGCCCTCAGCGCGGAGATTGATCGAATCAAGAAAGAAATGATAAC 377
 QY 301 ATGCAAGTACGCTCAGGCTATCTGAAGGAGAGATATCATCATTTGAACATGTAGAG 360
 Db 378 ATGAGATCGAGCTCAGGCTATCTGAAGGCGAGATCTGACTCATCTGCAACCAAGAG 437
 QY 361 CTGATGCGCTTAGAGGAGCACTTGAATGGCTTACAGTATCCGGACACAGAGTCC 420
 Db 438 TTGATCATGATTTGAGGAGCACTTGATATGAGTGCAGCGCTGATGAAAGAAACAGATG 497
 QY 421 AAGTTCTGTCACATGATGAGAGACATGGAAGGCACTGAGATGAGATGAAGCGCTC 480
 Db 498 GAGCACTACAGAGCTGATGAATCTGGCAAGATGCTGAGATGAGAACAGATTGCTC 557
 QY 481 ACTTATGAGCTGCAAAACACAGGAGATGAAATAAAGAGATCTGAGAACATGGAA 540
 Db 558 GCATTTAAATGCG---ATCAGCAAGATATTGCGCTGAACCGGAAATGAGGAGCTGAG 614
 QY 541 AATGGGTATCATCAGAGGCTGGGGAATCAACCAACACAGCAGCAGATACCTTTT 600
 Db 615 CTGTTTACCATCG-----GACAGGACTTTGACGCCAGATGCGGATC 659
 QY 601 GCCTTCGCGTGCAGCTTATTCAGCCAAATCTCCAGGAGAGATCTTAATTAGATATCT 660
 Db 660 ACGTTCGCGTGCAGCTACCCACCCCACTCCAGGAGAACAGTACGCGTTTAATCT 719

RESULT 10

ABK82085
 ID ABK82085 standard; cdna; 789 BP.

XX AC ABK82085;

XX DT 27-AUG-2002 (first entry)

XX DE DNA encoding novel floral meristem identity protein LpMADS1.

XX KW Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein; gene; ss.

XX OS Lolium perenne.

XX PN WO200233091-A1.

XX PD 25-APR-2002.

XX PF 17-OCT-2001; 2001WO-AU001311.

XX PR 19-OCT-2000; 2000AU-00000873.

XX PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.

XX PA (AGRE-) AGRESEARCH LTD.

PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;

XX WPI; 2002-454601/48.

XX P-PSDB; ABG60932.

XX New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.

XX Claim 3; Fig 27; 290pp; English.

XX The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.

CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence encodes a novel floral
 CC meristem identity protein involved in floral development and a potential
 CC target for manipulating plant life cycles

XX SQ Sequence 789 BP; 233 A; 207 C; 211 G; 138 T; 0 U; 0 Other;

Query Match 29.6%; Score 256.8; DB 6; Length 789;

Best Local Similarity 64.4%; Pred. No. 4.6e-55;

Matches 425; Conservative 0; Mismatches 217; Indels 18; Gaps 2;

QY 1 ATGGGACGTGGGAAGTTGAGATCAAGAGATTGAGAACTCAAGTACAGCGAGGTGACC 60
 Db 84 ATGGGCGCGGGAAGATCGAGATCAAGAGGATCGAGAACCAAGCAACCCAGGTGACC 143
 QY 61 TACTCCAGAGGAGGATGGATTATCAAGAGCAAGGAGAGATCACTGTTCTATGTAT 120
 Db 144 TTCTCCAGCGCAAGACCGGATCTCAAGAGCCAGGAGATCAGCGTGTCTCGGAC 203
 QY 121 GCTAAAGTATCTTATCATTTATCTAGCTCTGGGAGAGATGGTTGAATACTCGAGCCCT 180
 Db 204 GCCAGGTGCGGCTGCTGCTTCTCCAGCGCGGCAAGCTCTACGACTTCTGCTCCCC 263
 QY 181 TCACTACGCTGACAGAAATCTTGGCAAAATACATGGACAATCTGGGAGAGATTGTGG 240
 Db 264 AAGACATCGCTATCAAGAAATCTTGGAGAGTACAGACCAACTCCGGGAAGATCTGTGG 323
 QY 241 GATGCTAAGCATGAGAACCTCAGCAATGAAGTGAAGTAGAGTCAAGAAAGACAATGACAGC 300
 Db 324 GATGAGAAACACAGAGCCCTCAGCGCGGAGATTGATCGATCAAGAAAGAAATGATAAC 383
 QY 301 ATGCAAGTACAGCTCAGGATCTTGAGGAGAGAGATATCATCATTTGACCATGTAGAG 360
 Db 384 ATGCAAGTACAGCTCAGGCACTTTGAAAGGCGAAGATCTGAATCTCACTGCAACCAAGAG 443

RESULT 12

ABK82127
ID ABK82127 standard; cDNA; 1065 BP.

XX
AC ABK82127;

XX
DT 27-AUG-2002 (first entry)

DE DNA encoding novel floral meristem identity protein LpMADS2-3.

XX Ryegrass; fescue; MADS-box; MADS, MADS-like protein; CENTROSADIALIS; CEN;
 XX CEN-like protein; AP2AL2; AP2, AP2-like protein; HB, Homeo-box protein;
 KW HB-like protein; AP2AL2; AP2, AP2-like protein; HB, Homeo-box protein;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein; gene; ss.

OS Lolium perenne.

XX PN WO200233091-A1.

XX PD 25-APR-2002.

17-OCT-2001: 2001WO-AU001311.

19-OCT-2000; 2000AU-000000873; XX PR

XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.

XX
PI Spangenberg G, Sawbridge TI, Onq EK, Emmerling M;
(NAME) (ADDRESS) (CITY) (STATE) (ZIP)

WPI; 2002-454601/
P-PSDB; ABG60945.

XX New substantially purified or isolated polypeptide e.g., MADS-box,
PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
PT fescue species, useful for controlling plant life cycles and/or growth
PT phases.

PS Claim 3; Fig 72; 290pp; English.

The invention describes a substantially purified or isolated polypeptide (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like proteins, APEXAL2 (AP2) and AP2-like proteins, Homeo-box proteins (HB) and HB-like proteins, or their functionally active fragments or variants. Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a vector (IV) comprising (II), is useful for modifying plant life cycles and/or growth phases, flowering processes, flowering and/or plant architecture and/or flower and/or inflorescence development in a plant, which involves introducing (II), (III) or (IV) into the plant. The individual or simultaneous enhancement or downregulation of MADS-box gene activities may alter flower, embryo and seed development, e.g., enhance or inhibit embryo differentiation and growth or alter flower organ identity through conversion of one floral organ in another. Manipulation of CEN or HB activity in plants alters the control of phase change, flowering time and the number of leaves made before flowering. Manipulation of AP2 activity in plants alters flower organ identity through conversion of one floral organ in another, leads to a change in the number of floral organs and flowering architecture. Manipulation of flowering plant architecture has a wide range of applications such as: inducing male sterility for hybrid seed production; changing flower architecture for enhancing value of ornamentals; delaying flowering in forage grasses thus stopping the formation of less digestible stems and increasing herbage quality; altering flowering time allowing early maturing crops; delaying vegetative phase to increase biomass production; increasing branching to enhanced business in fruit trees; altering plant size e.g. shorter plant stature; and in blocking flowering and reducing release for allergenic pollen. This sequence encodes a novel floral

XX 25-FEB-2000; 2000EP-00301439.
PF 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 23-MAR-1999; 99US-0126284P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
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Query Match 28.8%; Score 250; DB 3; Length 909;
Best Local Similarity 67.5%; Pred. No. 2.6e-53;
Matches 382; Conservative 0; Mismatches 180; Indels 4; Gaps 2;

QY 1 ATGGAGCTGGGAGGTTGAGATCAAGAGATTGAGAACTCAAGTAAACAGGAGGTGACC 60
DB 84 ATGGGTAGAGGAAGATCGAGATAAGAGGATAGAGAACGCAACCAACAGAGTGGTGACG 143
QY 61 TACTCCAAAGAGGAGGATGGATTATCAAGAAAGCAAGAGATCACTGTTCTATGTGAT 120
DB 144 TTCTCAAAGAGGAGGATGGATTGTTGAGAGAGGCTAAAGAGATCACAGTTCTTTGTGAT 203
QY 121 GCTAAAGATCTCTTATCTATCTATCTAGCTCTGGGAAGATGGTGAATACAGCAGCTC 180
DB 204 GCAAAAGTTCCTCTCAATCTTTGCAAGTAATGGTAAGATGATGATTAATCTTTGCTCT 263
QY 181 TCAACTACGCTGACAGAAATCTTTGGCAAAATACCATGCAATCTGGGAAGAGTTGTGG 240
DB 264 TCCATGATCTTGGTGTATGTTGGACCAATACCAAGATTATCT-GGCACAACTATGG 322
QY 241 GATGCTAAGATGAGAACCTTCAGCAATGAAGTGGATAGATCAAGAAAGACAAATGACAGC 300
DB 323 GATGCTAAGATGAGAACCTTCAGCAATGAAGTGGATAGATCAAGAAAGACAAATGATAGC 382
QY 301 ATCAAGTACAGCTCAGGCAATCTGAAGGAGAGATATCACATCAATTTGAACCATGTAGAG 360
DB 383 TTACAACTGAGGCTCAGGCAATCTGAAGGAGAGATATCACATCAATTTGAACCATGTAGAG 442
QY 361 CTGATGCTTACAGGAGCACTTGAATAATGGCTTACAAAGTATCGGACCAAGAGTCC 420
DB 443 CTGATGCTTACAGGAGCACTTGAATAATGGCTTACAAAGTATCGGACCAAGAGTCC 502
QY 421 AAGTTCGTCACATGATGAGACAAATGGAAGGCACTGGAAGATGAGAAATGAGAAATGAG 480
DB 503 GAGATCTTATATCAAAAGGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAGAAATGAG 562
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481 ACTTATGAGCTGCAAAAACAAACAGGAGATGAAATAAAGAGATGTGAGAAACATGGAA 540
563 ACTTCCAGCTGC---AACCAAGGAGATGGCTATAGCAAGCAACGCAAGGAGGAATGATG 619
541 AATGGGTATCATCAGAGGAGCTGGG 566
620 ATGAGAGATCATGATGGCAGTTGG 645

RESULT 14
AAC46623
ID AAC46623 standard; DNA; 1004 BP.
XX AC AAC46623;
XX AC AAC46623;
DT 18-OCT-2000 (first entry)
DE Zea mays DNA fragment SEQ ID NO: 50816.
XX Hybridisation assay; Genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic; pathway;
KW promoter; termination sequence; corn; ss.
XX Zea mays subsp. mays.
XX EP1033405-A2.
PD 06-SEP-2000.
PF 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
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PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
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Query Match 27.3%; Score 236.8; DB 3; Length 1004;
Best Local Similarity 63.0%; Pred. No. 6e-50;
Matches 402; Conservative 0; Mismatches 227; Indels 9; Gaps 2;
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Qy 1 ATGGGACGTGGGAAGTTTGAGATCAAGAGGATTGAGAAGTCAAGTAACAGGCAGGTGACC 60

Db 163 ATGGGGCGCGCAAGATCGAGATCAAGAGGATCGAGAACTCTTACCACCGGCGAGGTGACC 222
 Qy 61 TACTCCAGAGGAGGAATGGGATTTATCAAGAGGCAAGGAGATCACTGTTCTTATGTGAT 120
 Db 223 TTCTCCAGCGCGGGCGGACTGGTCAAGAGGCAAGGAGATCGGCTGCTCTCGAC 282
 Qy 121 GCTAAAGTATCTTATCATTTATCTAGCTCTGGAGAGATGTTGAATCTGACGCCCT 180
 Db 283 GCGAGGTGCGGCGTCACTCTTCTCAGCGGCGGCAAGCTTATGACTACTCTCGCCC 342
 Qy 181 TCAACTACGCTGACAGAAATCTTGGCAAAATACATGGCAATCTCGGAAGATTTGTGG 240
 Db 343 AGGACCTCGTGTCCAGGATCTTGGAGAGTACAGACCACTCCGGGAAGATTTGTGG 402
 Qy 241 GATGCTAAGCATGAGAACCTTCAGCAATGAAGTGAAGTCAAGAAAGACAAATGACAGC 300
 Db 403 GGTGAGAGGACACAGAACTTGAAGTGAAGTCAAGAAAGACAAATGACAGC 360
 Qy 301 ATGCAAGTACAGCTCAGGCACTTGAAGGAGAGGATATCATCATTTGAACCATGTAGAG 360
 Db 463 ATGCAAGTACAGCTCAGGCACTTGAAGGAGAGGATATCATCATTTGAACCATGTAGAG 360
 Qy 361 CTGATGCGCTTAGAGGAGCACTTGAAGGAGAGGATATCATCATTTGAACCATGTAGAG 360
 Db 523 CTGATGCGCTTAGAGGAGCACTTGAAGGAGAGGATATCATCATTTGAACCATGTAGAG 360
 Qy 421 AAGTTGCTGACATGATGAGAGCAATGGAAGGCACTGGAAGTGAAGTGAAGTGAAGTGAAG 480
 Db 583 GACTACTGAGAGTGCACAGCAATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 642
 Qy 481 ACTTATGAGTGCACAAACACAGGAGATGAAATGAAGAGAGATGGAAGAGATGGAAGAG 540
 Db 643 ACTTTAGGATGC---ACCAACAGGCTGTTGATCTGAGCGGCGCATGAGGAGCTGGAG 699
 Qy 541 AATGGGTATCATGAGGAGGAGTGGGAACTACAAACACAGGAGGAGTACCTTTT 600
 Db 700 ACCGGATACCATGAGTCCAGC-----ACGACAGGGATTTATTTCCAGAGTCCGCTC 753
 Qy 601 GCCTTCGCGTGCAGCTATTCAGCCAAATCTCCAGGA 638
 Db 754 ACCTTCGGGTGAGCCACCAACACCCACCTGCAGGA 791

RESULT 15

ABK82090
 ID ABK82090 standard; cDNA; 592 BP.

AC ABK82090;

XX 27-AUG-2002 (first entry)

DE Novel floral meristem identity gene LpMADS1 contig #5.

XX Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTFORADIALIS; CEN;
 KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein; ss.

OS Lolium perenne.

XX W020023091-A1.

XX 25-APR-2002.

XX 17-OCT-2001; 2001WO-AU001311.

XX 19-OCT-2000; 2000AU-00000873.

XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.

PA (AGRE-) AGRESEARCH LTD.
 XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 PI WPI; 2002-454601/48.
 XX New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTFORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 XX Claim 3; Fig 29; 290pp; English.
 PS The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTFORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced business in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence represents a contig
 CC polynucleotide novel floral meristem identity protein involved in floral
 CC development and a potential target for manipulating plant life cycles
 XX SQ Sequence 592 BP; 177 A; 143 C; 161 G; 95 T; 0 U; 16 Other;

Query Match 27.2%; Score 236; DB 6; Length 592;

Best Local Similarity 66.7%; Pred. No. 7.9e-50;

Matches 329; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

Qy 1 ATGGGACGTGGGAGGTTGAGATCAAGAGGATTTGAGAACTCAAGTAAACGAGGAGTGAAC 60
 Db 84 ATGGGGCGGCGGAGATCGAGATCAAGAGGATCGAGAACCCAGAGCAACGCCAGGTGACC 143
 Qy 61 TACTCCAGAGGAGGAATGGGATATCAAGAGGCAAGAGATCACTGTTCTATGTGAT 120
 Db 144 TTCTCCAGGCGCAAGAACGGGATCCTCAAGAGGCCCAAGGAGATCAGCGTCTCTCGAC 203
 Qy 121 GCTAAAGTATCTTATCATTTTATTTAGCTCTGGGAAGATGTTGAATACTGACGCCCT 180
 Db 204 GCGGAGTGGCGTCTGCTGCTTCTCCAGCGCGGCAAGCTCTACGACTTCTGCTCCCC 263
 Qy 181 TCAACTACGCTGACAGAAATCTTGGCAAAATACCATGAGTCAAGAAAGCAATGACAGC 240
 Db 264 AAGACATCGGTATCAAGAAATCTTGGGAAGATGACAGCAACCACTCCGGGAAGTACTGTG 323
 Qy 241 GATGCTAAGCATGAGAACTTCAGCAATGAAGTGGATAGAGTCAAGAAAGCAATGACAGC 300
 Db 324 GATGAGBAACACAGAGGCTCAGCGGAGATTTGATCGAATCAAGAAAGAAATGATAAC 383
 Qy 301 ATGCAAGTACGCTCAGGCACTTGAAGGAGGAGGATATCATCATTTGAACCATGTAGAG 360
 Db 384 ATGCAATGAGCTCAGGCACTTGAAGGAGGAGGATATCATCATTTGAACCATGTAGAG 443

QY	361	CTGATGGCCTTAGAGGAGCACTTGAAAATGGCCTTACAAGTATCCGGGACAAGCAGTCC	420
Db	444	TTGATCATGATTGAGGAGCACTTGATAATGGACTGACAGGCTGCTGATGAAAAACAGATG	503
QY	421	AAGTTGTCGACATGATGAGAGACAAATGGAAAGGCACCTGGAAGATGAGAATAAGCGCTC	480
Db	504	GAGCACTACNACAGGCTGATGAAAACCTGCNNGATGCTNNAAAGATGANAACAAGTGTTC	563
QY	481	ACTTATGAGCTGC	493
Db	564	GNATTTAAACTGC	576

Search completed: September 25, 2004, 16:09:50
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GenCore version 5.1.6
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Run on: September 25, 2004, 14:17:32 ; Search time 3666.24 Seconds
(without alignments)
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:
1: gb_ba.*
2: gb_btg.*
3: gb_in.*
4: gb_ov.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
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40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	868	100.0	868	8	MDO291490
2	768.2	88.5	890	8	AB081092
3	358.8	41.3	967	8	AB038462
4	354.8	40.9	845	8	AF043255
5	354.2	40.8	875	8	BPE488589
6	350	40.3	3130	8	MDO291491
7	323.4	37.9	904	8	PHEBP3
8	323.4	37.9	971	8	PHPMADS2
9	296.8	34.2	768	8	NTGLOBOSA
10	296	34.1	761	8	AF230711
11	291.4	33.6	780	6	AJ36587
12	291.4	33.6	780	8	PETTRNSFA
13	288.4	33.2	814	8	AY173061
14	280.2	32.3	920	8	AF029976
15	278.8	32.1	807	8	AB079259
16	277.2	31.9	810	8	GHY9726
17	274.6	31.6	802	8	AF052862
18	274.2	31.6	876	8	AB094967
19	274	31.6	848	8	AY173069
20	273.4	31.5	842	8	DCA271148
21	267.6	30.8	894	8	AF052857
22	267.6	30.8	896	8	SLSLM2
23	267.4	30.8	801	8	AF335473
24	267.2	30.8	784	8	AY162865
25	266	30.6	786	8	AY162861
26	265.2	30.6	896	8	ATHMADSBOX
27	264.6	30.5	759	8	AF052861
28	264.6	30.5	959	8	AF230710
29	259.8	29.9	744	8	AF230708
30	259	29.8	822	8	AB071379
31	258	29.7	697	8	AY157725
32	256.6	29.6	786	8	AY162836
33	256.4	29.5	793	8	AY162860
34	256	29.5	790	8	AY162866
35	253.6	29.2	810	8	AY162837
36	252.2	29.1	791	8	AF052863
37	250	28.8	909	8	AY089002
38	249	28.7	800	8	AF230713
39	247.2	28.5	733	8	AF052864
40	244.2	28.1	801	8	AB071380
41	242.2	27.9	907	8	AB094985
42	239	27.5	888	8	AF134114
43	237	27.3	719	8	AB089155
44	235.8	27.2	768	8	AY162867
45	235.8	27.2	879	8	AF134115

ALIGNMENTS

RESULT 1
MDO291490
LOCUS Malus domestica mRNA for Pistillata MADS-box protein (pi Gene).
DEFINITION MDO291490
ACCESSION AJ291490
VERSION AJ291490.1 GI:12666532
KEYWORDS PI gene; Pistillata MADS-box protein.
SOURCE Malus x domestica (apple tree)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE 1
AUTHORS Yao, J., Dong, Y. and Morris, B.A.
TITLE Parthenocarpic apple fruit production conferred by transposon

MDO291490 868 bp mRNA linear PLN 02-FEB-2001
Malus domestica mRNA for Pistillata MADS-box protein (pi Gene).

Pred. No. is the number of results predicted by chance to have a

Best Local Similarity 99.0%; Pred. No. 5,6e-183;		Matches 773; Conservative 0; Mismatches 8; Indels 0; Gaps 0;	
QY	75	GAATGGGATTTATCAAGAAGCAAGAGATCACTGTTCTATGTGATGCTAAAGTATCTCT	134
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QY	135	TATCATTTATCTAGCTCTGGGAGATGTTGTAATCTCAGCCCTCAACTACGCTGAC	194
Db	61	TATCATTTATCTAGCTCTGGGAGATGTTGTAATCTCAGCCCTCAACTACGCTGAC	120
QY	195	AGAAATCTTGGCAAAATACCATGGACATCTGGGAAGAAGTTGTGGATGCTTAAGCATGA	254
Db	121	AGAAATCTTGGCAAAATACCATGGACATCTGGGAAGAAGTTGTGGATGCTTAAGCATGA	180
QY	255	GAACCTCAGCAATGAAGTGATGATCAAGATCAAGAAAGCAATGACAGATCAAGTACGCT	314
Db	181	GAACCTCAGCAATGAAGTGATGATGATCAAGATCAAGAAAGCAATGACAGATCAAGTACGCT	240
QY	315	CAGGCATCTCAAGGGAGAGGATATCATCATTTGAACCATGTAGAGCTGATGCCCTTAGA	374
Db	241	CAGGCATCTCAAGGGAGAGGATATCATCATTTGAACCATGTAGAGCTGATGCCCTTAGA	300
QY	375	GGAAAGCACTTGAATGGCTTCAAGATATCCGGGACAGCAATGCAAGTTCTGCACAT	434
Db	301	GGAAAGCACTTGAATGGCTTCAAGATATCCGGGACAGCAATGCAAGTTCTGCACAT	360
QY	435	GATGAGAGCAATGGAAGGCACTGGGAAGATGAGAAATGAAGCGCTCACTTATGAGCTGCA	494
Db	361	GATGAGAGCAATGGAAGGCACTGGGAAGATGAGAAATGAAGCGCTCACTTATGAGCTGCA	420
QY	495	AAAAACAACAGGAGATGAAATAAAGAGAGATGTGAGAAACATGGAAATGGGTATCATCA	554
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QY	555	GAGCAGCTGGGAACTACACACACACAGCAGCATACCTTTGCTTCGCGTGCA	614
Db	481	GAGCAGCTGGGAACTACACACACACAGCAGCATACCTTTGCTTCGCGTGCA	540
QY	615	GCCTATTTCAGCCAAATCTCCAGGAGAGAAATCTAATTAGATATATCTTTGCAATTTGCATGCT	674
Db	541	GCCTATTTCAGCCAAATCTCCAGGAGAGAAATCTAATTAGATATATCTTTGCAATTTGCATGCT	600
QY	675	CTTTCTAATAGTTATATATCTCTCAACCTCTCTCTCTTTTCATCTCTCAGAGATT	734
Db	601	CTTTCTAATAGTTATATATCTCTCAACCTCTCTCTCTTTTCATCTCTCAGAGATT	660
QY	735	CTTAAGTTTATGTCAGATTTTCCAAATGTTTGTATGGAATTAGCTTCGTTATGAGGCTTT	794
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QY	795	GTTGGAACCTTGTAATTAATTAAGCGGTGCAATGAACTCGGTTTGTGGGAAAAA	854
Db	721	GTTGGAACCTTGTAATTAATTAAGCGGTGCAATGAACTCGGTTTGTGGGAAAAA	780
QY	855	A 855	
Db	781	A 781	
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AB038462			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.			
REFERENCE			
1			

AUTHORS		Kitahara, K., Hirai, S., Fukui, H. and Matsumoto, S.	
TITLE		Rose MADS-box genes 'MASAKO Bp' and B3' homologous to class B floral identity genes	
JOURNAL		Plant Sci. 161, 549-557 (2001)	
REFERENCE		2 (bases 1 to 967)	
AUTHORS		Matsumoto, S., Hirai, S. and Kitahara, K.	
TITLE		Direct Submission	
JOURNAL		Submitted (16-FEB-2000) Shogo Matsumoto, Gifu University,	
		Department of Biology, Faculty of Education; 1-1, Yanagido, Gifu,	
		Gifu 501-1193, Japan (E-mail:shmatsum@cc.gifu-u.ac.jp,	
		Tel:+81-58-233-2257, Fax:+81-58-293-2207)	
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		/mol_type="mRNA"	
		/db_xref="taxon:74645"	
		/tissue type="young floral parts"	
		/note="Rosa rugosa Thunb. ex Murray"	
gene		1..967	
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CDS		104..715	
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		/note="14 a nucleotides"	
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Db	104	ATGGGAGGGGTAAAGATTGAGATTAGAGGATTGAAAATCAAGCAACAGGACGTGACC	163
QY	61	TACTCCAGAGGAGGAATGGGATTATCAAGAGGCAAAAGGAGATCACTGTTCTTATGTGAT	120
Db	164	TATTTCTAGAGAAAGATGGGATCATCAAAAGGCTAGGAAATCACTGTTCTTGTGAT	223
QY	121	GCTAAAGTATCTCTTATCATTTTCTAGCTCTGGGAAGATGTTGAAATGCTGCA---GC	177
Db	224	GCTAAGGTTCTCTTATTATCATTTGCTAGCTCTGGAAAAATGTTGAATCTGCGCGGC	283
QY	178	CCTTCAACTACGCTGACGAAATCTTGGACAAATACCATGGACAATCTGGGAAGAGTTG	237
Db	284	CCTCAGGAACCGGATGAAATCTTGGCAAAATACCATCTCAGCTCTGGAAGAGTTA	343
QY	238	TGGGATGCTAAGCATGAGAACCTCAGCAATGAAGTGGATAGAGTCAAGAAAGCAATGAC	297
Db	344	TGGGATGCCAAGCATGAGAACCTCTGCAATGAAGTGGATAGAGTCAAGAAAGCAATGAT	403
QY	298	AGCATCAAGTAGAGCTCAGGCATCTGAAGGAGAGGATATCACATCATTTGACCATGTA	357
Db	404	GGCATCAAAATTGAGCTTCGGCATTTGAAGGGGGAGAGACATACATCTCTGAACCATGTG	463
QY	358	GAGCTGATGGCCTTAGAGGAAGCACTTTGAAAATGGCCTTACAAGTATCCGGGACAGCAG	417
Db	464	GACCTGATGGCCTTAGAGGAAGCAATTTGAAAATGGCCTTGAAGTATCAGAGACAGATG	523
QY	418	TCCAAAGTCTGACATGATGAGAGCAATGGAAGGCACTGGAAGATGAGATAGCGC	477
Db	524	TCCAGTACATGACCGCGGTTAGAGAAAAATACAGAGCTCTGGAGACGAGAAATAGCGC	583
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Db      638 -----NACTACACACACACATCAGATACCT 664
QY      598 TTTCCTTCCTCCGCTGAGCCTTATTCAGCAATCTCAGGAGAGAAATCTTAAT 649
Db      665 TTTCCTTACGTGTCAGCCTTAATCAGCAATCTCAGCAGCAATGTAAT 716

RESULT 4
AF043255
LOCUS      Cucumis sativus MADS box protein 26 (CUM26) mRNA, complete cds.
DEFINITION
ACCESSION AF043255
VERSION    AF043255.1 GI:4105096
KEYWORDS
SOURCE     Cucumis sativus (cucumber)
ORGANISM   Cucumis sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
REFERENCE 1 (bases 1 to 845)
AUTHORS   Kater,M.M., Franken,J., Carney,K., van Lookeren Campagne,M.M. and
          Angenent,G.C.
TITLE     Class C homeotic genes are required for whorl specific sex
          determination in unisexual flowers
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 845)
AUTHORS   Kater,M.M., Franken,J., Carney,K., van Lookeren Campagne,M.M. and
          Angenent,G.C.
TITLE     Direct Submission
JOURNAL   Submitted (15-JAN-1998) Developm. Biology, CPRO-DLO,
          Droeveendaalsesteeg 1, Wageningen 6708 PB, The Netherlands
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            /note="class B MADS box gene"
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        40.9%; Score 354.8; DB 8; Length 845;
        Best Local Similarity 66.0%; Pred. No. 1.2e-78;
        Matches 568; Conservative 0; Mismatches 272; Indels 20; Gaps 3;

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        61 TACTCAAGAGGAGGAGGAGTATGATTAATCAAGAGGCAAGGAGATCACTGTTCTTATGTGAT 120
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        66 TATTCAAGAGAGAGAAATGGTATCATCAAAAAGCCAAAGAAATTAAGTCTTTTGGCAT 125
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Db      126 GCTCAAGTTTCTTGTTCATTTTCTGCTAGCTCTGGAAAAATGTCATGAATATTGACGCCCT 185
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Db      486 AACTATGAGCTGTACCAAAAGGAGATGGTTGCAATGGAGATAGTGTGAGAGAAATGAT 545
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Db      711 ATAATCTCTAGACTTTTAAAT-----TATGTGTACAAACTTTGGGTATGTGTATGT 765
QY      781 CGTTATGAGGCTTTGTTGTGAACCTTGTAAATAATTAGGCGTGCATGAATCGGTTTGTG 840
Db      766 TATTATGTAAGTCTTATGATGAGAACTCAATCACTGTTAAGCTAATGTTATGTATGTTA 825
QY      841 GGAAGAAAAAAGAAAAA 860
Db      826 ATAAAAAAGAAAAA 845

RESULT 5
BPE48589
LOCUS      Betula pendula mRNA for PISTILLATA homologue (mads2 gene).
DEFINITION
ACCESSION AJ488589
VERSION    AJ488589.1 GI:28874429
KEYWORDS   mads2 gene; PISTILLATA.
SOURCE     Betula pendula (European white birch)
ORGANISM   Betula pendula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fagales; Betulaceae; Betula.
REFERENCE 1
AUTHORS   Jarvinen,P., Lemmetyinen,J., Savolainen,O. and Sopanen,T.
TITLE     DNA sequence variation in BpMADS2 gene in two populations of Betula
          pendula
JOURNAL   Mol. Ecol. 12 (2), 369-384 (2003)
MEDLINE   22423798
PUBMED    12535088
REFERENCE 2 (bases 1 to 875)
AUTHORS   Jaervinen,P.L.H.
TITLE     Direct Submission

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JOURNAL Submitted (29-MAY-2002) Jaervinen P.L.H., Biology, University of Joensuu, P.O.Box 111, FIN-80101, Joensuu, FINLAND

FEATURES

source 1..875 /organism="Betula pendula" /mol_type="mrna" /db_xref="taxon:3505" /sex="male" /tissue_type="inflorescence" /country="Finland" 1..875 /gene="mads2" 1..636 /gene="mads2" /codon_start=1 /product="PISTILLATA homologue" /protein_id="CAD32764.1" /db_xref="GI:28874430" /translation="MGRGKIEIKRIENSNROVTVSKRMKGIKKAKESILCDKAVP LVIFSSGKMKYECSPSTLTILDMYHKRSKRLWDKAKHENLSNEVDVRVKDNDMSQ IELRHMKGEDITSLNHRELMLEALONGHSSIREROMDLMRAKKDKILKEENKCL NFTLHQQVAMEAASCRDVEDDYEQVRDYNQMPFAFRVQPIQPNLQDRM"

ORIGIN

Query Match 40.8%; Score 354.2; DB 8; Length 875; Best Local Similarity 73.0%; Pred. NO. 1.7e-78; Matches 474; Conservative 0; Mismatches 163; Indels 12; Gaps 1; QY 1 ATGGGAGCTGGGAAGGTTGAGATCAAGAGGATTGAACTCAAGTAACAGGAGGTGACC 60 Db 1 ATGGGAGGAAAGATAGAGATAAGAGGATAGAGACTCAAGTAACAGGAGGTGACC 60 QY 61 TACTCCAAGAGGAGGAATGGGATATCAAGAGGCAAGAGATCACTCTTATGTGAT 120 Db 61 TACTCAAGAGGATGAAGGGGATCATAAGAGAGGCTAAGAGATCAAGCATCTTATGTGAT 120 QY 121 GCTAAAGTATCTCTTATCACTTATCTAGCTCTGGCAAGATGTTGTAATCTCGACCCCT 180 Db 121 GCTAAAGTCTCTTGTATCTTTGACAGCTCAGGAAGATGAAGAGTACTCGACCCCT 180 QY 181 TCAACTACGCTGACAGAAATCTTGGCAAAATCAATGGAACAATCTGGGAAGAGTTGTGG 240 Db 181 TCAACTACGCTGATTAACATCTTGGACATGTACCAAGCGGTCTGAGAAGAGATTGTGG 240 QY 241 GATGCTTAGCATGAGACCTCAGCAATGAGTGTAGTCAAGAGTCAAGAGACATGACAGC 300 Db 241 GATGCCCAACATGAGAACCTCAGCAATGAATTTCTAGAAATCAAGAAAGAGACGACAC 300 QY 301 ATGCAAGTAGAGCTCAGGCATCTGAAGGAGAGATATCATCATTTGAACCATGTAGAG 360 Db 301 ATGCAGATTGAATCAGGCATGAGAGGGGAGGATATCATCTTTGAACCATGAGAG 360 QY 361 CTGATGCCCTTAGAGGAGCACTTGAATATGGCTTACAGATATCCGGACACGAGTCC 420 Db 361 CTGATGATCTCTGAGGAGGCTTCAAAATGGCCACAGCAGTATCCGCGAGGCGAGATG 420 QY 421 AAGTTCTGACATGATGAGAGCAATGGAAAGGCACTGGAAGATGAGAATAAGCGCCTC 480 Db 421 GACTTATGATGAGCTAGGAAAAGACAGATCTTGGAGGAGGAGATAGTGCCTT 480 QY 481 ACTTATGAGCTGCAAAAACACAGGAGATGAAAATAAAGAGATGTGAGAAACATGGAA 540 Db 481 AATTCTACTCTGATCAGCAGCAGATGGCATGGAAGCAGCAAGCTGCAGAGACGTGGAA 540 QY 541 AATGGGTATCATCAGAGGAGCTGGGAACTACACCAACACAGCAGCAGATACCTTTT 600 Db 541 GATGATTTATGAGCAGAGGAGGTGAGG-----ACTAATATCTCAATGTCCTTTT 588 QY 601 GCCTTCGCGTGCAGCCTTATTCAGCCAAATCTCAGGAGAGAAATCTAAT 649 Db 589 GCTTTCGCGTGCAGCCTTATTCAGCCAAATCTCAGGATAGATGATTAAT 637

RESULT 6

MDO291491 LOCUS

DEFINITION Malus domestica pi gene for Pistillata MADS-box protein, exons 1-7.

ACCESSION AJ291491

VERSION 1

KEYWORDS PI gene; Pistillata MADS-box protein; transcription factor.

SOURCE Malus x domestica

ORGANISM Malus x domestica

REFERENCE 1

AUTHORS Yao, J., Dong, Y. and Morris, B.A.

TITLE Parthenocarpic apple fruit production conferred by transposon insertion mutations in a MADS-box transcription factor

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (3), 1306-1311 (2001)

MEDLINE 21107711

PUBMED 11158635

REFERENCE 2

AUTHORS Yao, J.L.

TITLE Direct Submission

JOURNAL Submitted (16-OCT-2000) Yao J.L., Plant Health and Development Group, Horticulture and Food Research Institute of New Zealand, 120 Mt Albert Road, Auckland, Private Bag 92169, NEW ZEALAND

FEATURES

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CDS /cultivar="Granny Smith"

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Query Match      40.3%; Score 350; DB 8; Length 3130;
Best Local Similarity 98.6%; Pred. No. 2e-77;
Matches 353; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 2773 TGAATTCGACAAACACACAGGAGATGAAATAGAGAGAAATGTGAGAAACATGGAATA 2832

Qy 543 TGGGTATCATCAGAGGAGCTGGGAACTACAAACAACACCAGCAGATACCTTTTGC 602
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Qy 603 CTTCCGGCTCAGCCTATTGAGCAATCTCCAGGAGAAATCTAATAGATATATCTTG 662
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Qy 663 CATTTGCATCTCTTTCTAACTAGTTATATATCTCTCACTCTCTCTCTCTCTCTCTC 722
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Qy 723 TGTCAAGAGTCTTAAAGTTATGTCAGATTTCCAAATGTTGTAATGAAATAGCTTCG 782
Db 3013 TGTCAAGAGTCTTAAAGTTATGTCAGATTTCCAAATGTTGTAATGAAATAGCTTCG 3072

Qy 783 TTATGAGGCTTCTGTTGAACCTTGTAAATATTAAGCGGTGATGAATCGGTTTGTG 840
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RESULT 7
PHFBP3
LOCUS      P.hybrida fbp3 mRNA.
DEFINITION X71417
ACCESSION X71417
VERSION    X71417.1 GI:454264
KEYWORDS   fbp3 gene; MADS-box protein.
SOURCE     Petunia x hybrida
ORGANISM   Petunia x hybrida
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamids; Solanales; Solanaceae; Petunia.

REFERENCE
AUTHORS    Angenent,G.C., Franken,J., Busscher,M., Weiss,D. and van Tunen,A.J.
TITLE       Co-suppression of the petunia homeotic gene fbp2 affects the
            identity of the generative meristem
JOURNAL     Plant J. 5 (1), 33-44 (1994).
MEDLINE     9417174
PUBMED     7907515
REFERENCE   2 (bases 1 to 904)
AUTHORS    Angenent,G.C.
TITLE       Direct Submission
JOURNAL     Submitted (30-MAR-1993) G.C. Angenent, CPRO-DLO, Droeendaalsesteeg
            1, Wageningen, THE NETHERLANDS
FEATURES    Location/Qualifiers

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ORIGIN
Query Match      37.9%; Score 329.4; DB 8; Length 904;
Best Local Similarity 70.6%; Pred. No. 3e-72;
Matches 457; Conservative 0; Mismatches 181; Indels 9; Gaps 1;

Qy 1 ATGGGAGCTGGGAAGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACAGGAGGTGACC 60
Db 46 ATGGGAGAGGAAGATAGAGATTAAGAGATAGAGAACTCTAGCAACAGGCAAGTTACT 105

Qy 61 TACTCCAAAGAGGAGAAATGGGATTATCAAGAGGCAAAAGGAGATCACTGTTTCTATGAT 120
Db 106 TACTCCAAAGAGAGAAATGGGATTATCAAGAGGCAAAAGGAGATCACTGTTTCTATGAT 165

Qy 121 GCTAAAGTATCTCTTATCATTTTCTAGCTCTGGGAAGATGTTGTAATTAAGTACTGACGCC 180
Db 166 GCTAAAGTATCTCTTATCATTTTCTAGCTCTGGGAAGATGTTGTAATTAAGTACTGACGCC 225

Qy 181 TCAACTACGTCAGAGAAATCTTGGACAAATACCATGGACAAATCTGGGAAGAGTTGTGG 240
Db 226 TCTACTACGTTACTGATATGCTGGATGTTATCAAAAACCTCTGGGAGGAGGCTATGG 285

Qy 241 GATGCTAAGCATGAGAACCTCAGCAATGAGTGGATAGAGTCAAGAGACATGACAGC 300
Db 286 GATGCTAAGCATGAGAACCTCAGCAATGAGTGGATAGAGTCAAGAGACATGACAGC 345

Qy 301 ATGCAAGTAGAGCTCAGGCATCTGAAAGGGAGAGGATATCACATCATTTGAACCATGTAGAG 360
Db 346 ATGCAAGTTAAGCTCAGGCACCTCAAAGGAGAGATATCAATTTCTTTGAACCAAGAG 405

Qy 361 CTGATGSCCTTAGAGGAGCACTTGAATATGSCCTTACAGATATCCGGGACAGAGCTTC 420
Db 406 CTTATGGTTTGGGAAGAGGCTTAAACAAATGGACITTTCTAGTATCAAGTCCAGGAGCTCG 465

Qy 421 AAGTTGCTGCACATGATGAGAGCAATGGAAGGCACTGGAAGATGAGAAATAGAGCCCTC 480
Db 466 GAGATCTTGAGGATAGTCAGGAATATGATCAAAATCTGGAGGAGGAACAACAAGCACTT 525

Qy 481 ACTTATGAGCTGCAAAAACAACAGGAGATGAAATATAAAGAGAGATGTGAGAACATGGAA 540
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Qy 541 AATGGGTATCATCAGAGGAGCTGGGGAACCTACAAACAACACAGCAGAGATACCTTTT 600
Db 586 GAAGTGATACCAAGAGACAGG-----ATTACGAATACAGAGAGATGCCATTT 636

Qy 601 GCCTTCGGGTGAGCCTTATTCAGCCAAATCTCCAGGAGAGATCTA 647
Db 637 GCCCTTCGAGTTTCAGCCAAATTCAGCCAAATCTACATGAAAGAAATGTA 683

RESULT 8
PHPMDS2

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LOCUS PHPMADS2 971 bp mRNA linear PLN 06-OCT-1994
DEFINITION P.hybrida mRNA for pmads 2.
ACCESSION X69947
VERSION X69947.1 GI:22666
KEYWORDS developmental gene; DNA-binding transcription factor; MADS-box
protein; pmads2 gene.
SOURCE Petunia x hybrida
ORGANISM Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Petunia.
1 (bases 1 to 971)
Kush, A., Brunelle, A., Shevell, D. and Chua, N.H.
The cDNA sequence of two MADS box proteins in Petunia
Plant Physiol. 102 (3), 1051-1052 (1993)
94105323
MEDLINE 8278527
PUBMED
REFERENCE 2 (bases 1 to 971)
Brunelle, A.N.
Direct Submission
AUTHORS
TITLE Submitted (23-NOV-1992) A.N. Brunelle, The Rockefeller University,
JOURNAL Dept of Plant Molecular Biology, 1230 York Avenue, New York, NY
10021, USA
COMMENT The MADS transcription factor open reading frame is very similar to
the GLO protein from Antirrhinum majus.
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Query Match 37.9%; Score 329.4; DB 8; Length 971;
Best Local Similarity 70.6%; Pred. No. 3e-72;
Matches 457; Conservative 0; Mismatches 181; Indels 9; Gaps 1;
QY 1 ATGGGAGCTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAACAGGCGAGTGACC 60
DB 45 ATGGGAGAGAAAGATAGATTAAGAGATAGAGACACTAGACACAGGCAAGTTACT 104
QY 61 TACTCCAAAGAGAGAAATGGGATTATCAAGAAAGCAAGAGATCATCTGTTCTATGTAT 120
DB 105 TACTCCAAAGAGAGAAATGGGATTATCAAGAAAGCTAAAGAAATCACTGTTCTTTGTAT 164
QY 121 GCTAAGATATCTTATCATTTATCTAGCTCTGGGAGATGGTTGAATCTGCAGCCCT 180
DB 165 GCTAAGGTTTCCCTTATCATCTTTGGTAATTTCTGGCAGATGCAATGATTTGTAGCCCT 224
QY 181 TCACTACGCTGACAGAAATCTTGGACAAATACCATGGACAAATCTGGGAAGAAGTTGTGG 240
DB 225 TCTACTAGTTTACCTGATATGCTGGATGTTATCAAAAACTTCTGGGAGGAGGCTATGG 284
QY 241 GATGCTAAGCATGAGAACTCAGCAATCAAGTGAATGATAGATCAAGAAAGCAATGACAGC 300
DB 285 GATGCTAAGCATGAGAACTGAGCAATGAAATCGATAGATCAAGAAAGCAATGACAAAT 344

QY 301 ATGCAAGTAGAGCTCAGGCATCTGAAGGAGAGATATCATCATTTGAACCATGTAGAG 360
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DB 525 CAATATGCTTTGCACCAAAAGAGATGGCGCCATGGTGGAAATATGAGAAATGATTGAA 584
QY 541 AATGGTATCATCAGAGCAGCTGGGAACTACACCAACCAACAGCAGCAGATACCTTTT 600
DB 585 GAATGTACCAATCAAGAGACAGG-----ATTACGATACAGCAGATGCCATTT 635
QY 601 GCCTTCCGCTGCGCCTTATTCAGCCAAATCTCCAGGAGAGAATCTA 647
DB 636 GCCTTCGAGTTCAGCAATGCAGCAATCTACATGAAGAATGTA 682

RESULT 9
NTGLOBOSA 768 bp mRNA linear PLN 10-JUN-1993
LOCUS N.tabacum GLO mRNA.
DEFINITION X67959
ACCESSION X67959
VERSION X67959.1 GI:19870
KEYWORDS DNA binding protein; transcription factor.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
REFERENCE 1 (bases 1 to 768)
AUTHORS Hansen, G., Eistrich, J.J., Sommer, H. and Spena, A.
TITLE NTGLO: a tobacco homologue of the GLOBOSA floral homeotic gene of
Antirrhinum majus: cDNA sequence and expression pattern
JOURNAL Mol. Gen. Genet. 239 (1-2), 310-312 (1993)
MEDLINE 93288002
PUBMED 8095711
REFERENCE 2 (bases 1 to 768)
AUTHORS Hansen, G.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1992) G. Hansen, Max-Planck Inst. fuer
Zuchtungsforshung, Carl-von-Linne Weg, 10, 5000 Koeln 30, FRG
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ORIGIN

Query Match 34.2%; Score 296.8; DB 8; Length 768;
 Best Local Similarity 68.2%; Pred. No. 5.1e-64;
 Matches 450; Conservative 0; Mismatches 192; Indels 18; Gaps 2;

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QY 61 TACTCCAAAGAGAGGAATGGGATATCAAGAGGCAAGAGAGATCACTGTTCTATGTGAT 120
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QY 121 GCTAAAGTATCTTATCAATTTATCTAGCTCTGGGAAGATGTTGAATCTCAGCCCT 180
 DB 121 GCTCGTGTCTGTCATCAATTTTGTAGTTCTGGCAAGATGCATGATCTCT-----CC 174

QY 181 TCAACTACGCTGACAGAAATCTTGCACAAATACCATGCAATCTGGGAGAGTTGTGG 240
 DB 175 TCTACTTCTGTTGTTGATATTTTGGATCAATACCAAGCTTACTGGAAGAGATTGTGG 234

QY 241 GATCTAAGCATGAGAACCTTCAGCAATGAAGTGGATAGAGTCAAGAAAGACAAATGACAG 300
 DB 235 GATCTAAGCATGAGAACCTTGGCAATGAATCAACAAAGTCAAGAAAGACAAATGACAAAC 294

QY 301 ATGCAAGTACGCTCAGGCATCTGAAGGAGAGAGATATCACTATGTAACCATGTAGAG 360
 DB 295 ATGCAAAATTGAATCAGGCACCTTAAAGGGTGAAGACATCACTCTTTGAACCAAGAGAG 354

QY 361 CTGATGCGCTTAGAGGAAGACCTTGAATGGGCTTACAAAGTATCCGGACAGAGATCC 420
 DB 355 CTGATGATGTTGAAGATGCGCTTGTATATGGACTCACTAGTATCCGTACAGAGAAAT 414

QY 421 AAGTTCGTACATGATGAGAGCAATGGAAGGCACTGGAAGATGAGAAATGAAGCCCTC 480
 DB 415 GACCTTCTGAGGATGATGAGGAAAAAGACTCAAAGTATGGAGGAGCAAGACCAACTT 474

QY 481 ACTTATCAGCTGCAAAACCAAGAGAGATGAAATAAAGAGAACTGTGAAGAACATGGAA 540
 DB 475 AATTGGCAATTGGGCACTAGAGATAGCAAGTATGATAGGATATGGAGAAATAGGG 534

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 DB 535 GAAAGTGTTCACCAAGGGAG-----AATGAATACCAAACTCAGATGCTTTT 582

QY 601 GCCTTCGCGTGCAGCTATTCAGCAAAATCTCCAGAGAGATCTTAATTAGATATATCT 660
 DB 583 GCCTTCGAGTTCAGCAATGCGACCTAATTTGAGAGAGATTTTAAACACCTTGATTT 642

RESULT 10
 AF230711
 LOCUS
 DEFINITION Hydrangea macrophylla MADS box containing protein PI mRNA, partial cds.

ACCESSION AF230711
 VERSION AF230711.1
 KEYWORDS GI:8163963

SOURCE Hydrangea macrophylla
 ORGANISM Hydrangea macrophylla
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; Cornales; Hydrangeaceae; Hydrangea.

REFERENCE 1 (bases 1 to 761)
 Kramers, E.M. and Irish, V.F.
 Evolution of the petal and stamen developmental programs: Evidence from comparative studies of the lower eudicots and basal angiosperms
 Int. J. Plant Sci. (2000) In press

REFERENCE 2 (bases 1 to 761)
 Kramers, E.M. and Irish, V.F.
 Direct Submission
 TITLE Submitted (03-FEB-2000) MCDB, Yale University, PO Box 208104, New Haven, CT 06511-8104, USA

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Query Match 34.1%; Score 296; DB 8; Length 761;
 Best Local Similarity 71.3%; Pred. No. 8e-64;
 Matches 462; Conservative 0; Mismatches 150; Indels 36; Gaps 4;

QY 76 AATGGGATATCAAGAGGCAAGGAGATCACTGTTCTATGTGATGCTAAAGTATCTTT 135
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QY 256 AACCTCAGCAATGAAGTGGATAGAGTCAAGAAAGACAATGACAGCATGCAAGTAGAGCTC 315
 DB 181 AATCTCAGCAATGAATTTGATAGATCAAGAAAGAGAACGTAACATGAGATTGAGCTA 240

QY 316 AGGATCTGAAGGAGAGGATATCAATCATTTGAAACCATGTAGAGCTGATGGCTTAGAG 375
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QY 376 GAAGCACTTGAAATGGCTTTACAAGTATCCGGACAAGCAGTCCAAGTTCTGTCGACATG 435
 DB 301 CTAGCCCTTGAGAAATGGCTTTGCTAGTATTCGTGACAGAAAGGATGAGGTTCTCGAGATG 360

QY 436 ATGAGAGCAATGGAA-----AGGCATCGAAGATGAGAAATGAAGCCCTCACTTATGAG 489
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QY 550 CATCAGAGGAGCTGGGAACTACAACAACCAAGCAGCAGATACCTTTTGGCTTTCCGC 609
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QY 610 GTCGAGCTATTCCAGCAATCTCCAGGAGAGATCTAATTAGATATATCTTGCATTCG 669
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QY 670 ATGCTCTTTCTAACTAGTTATATATCTCTCCACCTCTCTCTCTCTCTCT 717
 DB 571 ATGTTGAGCTTAATTAGCTGAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 618

RESULT 11

A36587
 LOCUS
 DEFINITION Sequence 1 from Patent WO9400582.
 ACCESSION A36587
 VERSION A36587.1
 GI:2293891

linear
 DNA
 780 bp
 PAT 05-MAR-1997

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KEYWORDS      Petunia x hybrida
SOURCE        Petunia x hybrida
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              asterids; lamids; Solanales; Solanaceae; Petunia.

REFERENCE     Van, T.A., Mollena, C., Angenent, G.C. and Dons, J.J.
AUTHORS       A METHOD FOR OBTAINING A PLANT HAVING ALTERED FLORAL MORPHOLOGY AND
TITLE         A METHOD FOR PROTECTING PLANTS AGAINST PEST INSECTS
JOURNAL       Patent: WO 940582-A 1 06-JAN-1994;
              FOR PLANT BREEDING AND REPRODU (NL)
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               QY 1 ATGGGACGTGGGAGGTTGAGATCAAGAGATTGAGAACTCAAGTAAACAGCGAGTGACC 60
               DB 8 ATGGGAGAGGAAAGATAGAGATAAAGAAATAGAAAACTCAAGCAACAGACAACTAACT 67
               QY 61 TACTCCAGAGGAGGAGTGGATATCAAGAGGCAAGAGATCACTGTTCTATGTGAT 120
               DB 68 TACTCAAAAAGAGAAATGGGATCTTGAAAAAGCTTAGGAAATTTAGTGTCTTTGTGAT 127
               QY 121 GCTAAAGTATCTTATCATTTTATCTAGCTCTCGGAAAGATGGTTGAATATCTGCAGCCCT 180
               DB 128 GCTCGTGTCTGTTATCATTTTCTAGCTCTCGGAAAGATGCATGAGTTCT-----CT 181
               QY 181 TCAACTACGCTGACAGAAATCTTGACAAATACCATGGACATCTGGGAAGAGTGTG 240

               Query Match      33.6%; Score 291.4; DB 8; Length 780;
               Best Local Similarity 67.8%; Pred. No. 1.2e-62;
               Matches 444; Conservative 0; Mismatches 196; Indels 15; Gaps 2;

               QY 1 ATGGGACGTGGGAGGTTGAGATCAAGAGATTGAGAACTCAAGTAAACAGCGAGTGACC 60
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               QY 181 TCAACTACGCTGACAGAAATCTTGGAACAATACCATGGCAATCTGGGAAGAGTGTG 240
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               QY 421 AAGTTCGTCGATGATGAGAGCAATGGAAGGCACTGGAAGATGAGAAATAGCGCCTC 480
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482 AATTGCCAATTGCGCAACTTGAGATAGCAACCATGAATAGGAATATGGGAGAAATTGGC 541
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542 GAAGTGTTCAGCAGAGGAG-----AATCATGATACCAAAACCATATCCCTTTT 592
601 GCCTTCGCGTGCAGCCCTATTTCAGCCAAATCTCCAGAGAGAAATCTAATTAGATA 655
593 GCCTTCGAGTACAAACCAATGCAAGCAATTTGAGGAGAGGTTGTAAAAAAGA 647

RESULT 12
LOCUS   PETRNSFA
DEFINITION Petunia transcription factor (fbp1) RNA, complete cds.
VERSION M91190.1 GI:169253
KEYWORDS transcription factor.
SOURCE  Petunia x hybrida
ORGANISM Petunia x hybrida
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          asterids; lamids; Solanales; Solanaceae; Petunia.
          1 (bases 1 to 780)
REFERENCE Angenent, G.C., Busscher, M., Franken, J., Mol, J.N. and van Tunen, A.J.
AUTHORS   Differential expression of two MADS box genes in wild-type and
TITLE     mutant petunia flowers
JOURNAL   Plant Cell 4 (8), 983-993 (1992)
MEDLINE   93005737
PUBMED    1356537
COMMENT   Original source text: Petunia hybrida (strain R27) flower petals
          and stamen cDNA to mRNA.
FEATURES  Location/Qualifiers
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ORIGIN
Query Match      33.6%; Score 291.4; DB 8; Length 780;
Best Local Similarity 67.8%; Pred. No. 1.2e-62;
Matches 444; Conservative 0; Mismatches 196; Indels 15; Gaps 2;

QY 1 ATGGGACGTGGGAGGTTGAGATCAAGAGATTGAGAACTCAAGTAAACAGCGAGTGACC 60
DB 8 ATGGGAGAGGAAAGATAGAGATAAAGAAATAGAAAACTCAAGCAACAGACAACTAACT 67
QY 61 TACTCCAGAGGAGGAGTGGATATCAAGAGGCAAGAGATCACTGTTCTATGTGAT 120
DB 68 TACTCAAAAAGAGAAATGGGATCTTGAAAAAGCTTAGGAAATTTAGTGTCTTTGTGAT 127
QY 121 GCTAAAGTATCTTATCATTTTATCTAGCTCTCGGAAAGATGGTTGAATATCTGCAGCCCT 180
DB 128 GCTCGTGTCTGTTATCATTTTCTAGCTCTCGGAAAGATGCATGAGTTCT-----CT 181
QY 181 TCAACTACGCTGACAGAAATCTTGGAACAATACCATGGACATCTGGGAAGAGTGTG 240

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RESULT 13

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 DEFINITION (cdm86) mRNA, complete cds.
 ACCESSION AV173061
 VERSION AV173061.1 GI:27804368

KEYWORDS Chrysanthemum x morifolium (Dendrathera grandiflora)

SOURCE

ORGANISM Chrysanthemum x morifolium

REFERENCE 1 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 2 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 3 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 4 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 5 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 6 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 7 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 8 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 9 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 10 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 11 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 12 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 13 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 14 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 15 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 16 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 17 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 18 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 19 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 20 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 21 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 22 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 23 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 24 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 25 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 26 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
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 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 28 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

REFERENCE 29 (bases 1 to 814)
 Schennikov, A.V., Shulga, O.A., Skryabin, K.G. and Angenent, G.C.
 Submitted (05-NOV-2002) Plant Development and Reproduction. Plant Research International, Drosendaalsesteeg 1, Wageningen 6700 AA, The Netherlands

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 Matches 367; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

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 Qy 481 ACTTATGAGCTGCAAAAA 498
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RESULT 14

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LOCUS Eucalyptus grandis MADS box protein (EGM2) mRNA, complete cds.

DEFINITION AF029976

ACCESSION AF029976

VERSION AF029976.1 GI:3114585

KEYWORDS Eucalyptus grandis

SOURCE Eucalyptus grandis

ORGANISM Eucalyptus grandis

REFERENCE 1 (bases 1 to 920)

Southern, S.G., Marshall, H., Mouradov, A. and Teasdale, R.D.

Submitted (16-OCT-1997) Biochemistry, University of Queensland, St Lucia, Queensland 4072, Australia

Location/Qualifiers

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source

REFERENCE 2 (bases 1 to 920)

Southern, S.G., Marshall, H.O. and Teasdale, R.D.

Submitted (16-OCT-1997) Biochemistry, University of Queensland, St Lucia, Queensland 4072, Australia

Location/Qualifiers

1. .920

source

REFERENCE 3 (bases 1 to 920)

Southern, S.G., Marshall, H.O. and Teasdale, R.D.

Submitted (16-OCT-1997) Biochemistry, University of Queensland, St Lucia, Queensland 4072, Australia

Location/Qualifiers

1. .920

source

FEATURES

source

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Best Local Similarity 69.3%; Pred. No. 7.9e-60;
Matches 397; Conservative 0; Mismatches 173; Indels 3; Gaps 1;

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QY 121 GCTAAAGTATCTTATCATTTATCTAGCTCTGGGAAGATGTTGAATACTGCAGCCT 180
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QY 301 ATGCAAGTAGAGCTCAGGCATCTGAAGGAGAGGATATCAATCATTTGAACCATGTAG 360
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DB 590 GACGGTTACCATCAAGANTGAAGGCTGACTTC 622

RESULT 15
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LOCUS AB079259 807 bp mRNA linear PLN 02-APR-2003
DEFINITION Agapanthus praecox ApMADS1 mRNA for MADS-box transcription factor
PI, complete cds.
ACCESSION AB079259
VERSION AB079259.1 GI:29467045
KEYWORDS Agapanthus praecox
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
Asparagaceae; Agapanthus.
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AUTHORS Nakamura,T. and Nakano,M.
TITLE The MADS-box gene which expressed in floral organs of Agapanthus
praecox
JOURNAL Published Only in Database (2003)
REFERENCE 2 (bases 1 to 807)
AUTHORS Nakamura,T. and Nakano,M.
TITLE Direct Submission
JOURNAL Submitted (02-FEB-2002) Toru Nakamura, Niigata University, Fac. of
Agriculture, 2-8050 Ikarashi, Niigata, Niigata 950-2181, Japan
(E-mail: f01e402kemail.cc.niigata-u.ac.jp, Tel.81-25-262-6598,
Fax:81-25-262-6858)
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ORIGIN
Query Match 32.1%; Score 278.8; DB 8; Length 807;
Best Local Similarity 64.1%; Pred. No. 1.8e-59;
Matches 459; Conservative 0; Mismatches 242; Indels 15; Gaps 2;

QY 1 ATGGGACGTGGGAAGTTGAGATCAAGAGGATTGAGAACTCAAGTAAACGCGCAGGTGACC 60
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3	314	25.8	84	5	PCR-U933-08386-14	Sequence 14, Appli
4	313	25.7	84	5	PCR-U933-08386-16	Sequence 16, Appli
5	295	24.3	249	2	US-08-867-087B-15	Sequence 15, Appli
6	290	23.8	241	2	US-08-867-087B-11	Sequence 11, Appli
7	287	23.6	248	2	US-08-867-087B-17	Sequence 17, Appli
8	285	23.4	285	4	US-09-611-635A-4	Sequence 4, Appli
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11	280	23.0	242	3	US-09-349-677-2	Sequence 2, Appli
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20	271	22.3	273	3	US-08-655-237-8	Sequence 8, Appli
21	271	22.3	273	3	US-08-655-241-8	Sequence 8, Appli
22	271	22.3	273	3	US-09-149-976-8	Sequence 8, Appli
23	271	22.3	273	4	US-09-398-326-8	Sequence 8, Appli
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; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
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; APPLICATION NUMBER: PCT/US93/08386
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/939,898
; FILING DATE: 04 SEP 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/088001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84
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; TOPOLOGY: linear
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RESULT 3
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; GENERAL INFORMATION:
; APPLICANT: Bernardo Nadal-Ginard
; TITLE OF INVENTION: MYOCYTE-SPECIFIC
; TITLE OF INVENTION: TRANSCRIPTION
; TITLE OF INVENTION: ENHANCING FACTOR 2
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: PCT/US93/08386
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/939,898
; FILING DATE: 04 SEP 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/088001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; PCT-US93-08386-14

```

```

Query Match 25.8%; Score 314; DB 5; Length 84;
Best Local Similarity 70.7%; Pred. No. 1.3e-23;
Matches 58; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

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QY 4 GKIEIKLIENQTNRQVTSYKERNGIFKKAQELTVLCDAKVSIMLSNTNKHHEYISPTT 63
Db 2 GKIEIKLIENQTNRQVTSYKERNGIFKKAQELTVLCDAKVSIMISSTQKLHEYISPTT 61

QY 64 TTKSMYDDYQKTMGIDLWTHREE 85
Db 62 TTKRMIDYQKALGVDLWSSHYE 83

```

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RESULT 4
PCT-US93-08386-16
; Sequence 16, Application PC/TUS9308386
; GENERAL INFORMATION:
; APPLICANT: Bernardo Nadal-Ginard
; TITLE OF INVENTION: MYOCYTE-SPECIFIC
; TITLE OF INVENTION: TRANSCRIPTION
; TITLE OF INVENTION: ENHANCING FACTOR 2
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08386
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/939,898
; FILING DATE: 04 SEP 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/088001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:

```

LENGTH: 84
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-08386-16

Query Match 25.7%; Score 313; DB 5; Length 84;
Best Local Similarity 71.1%; Pred. No. 1.6e-23;
Matches 59; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 3 RGKIEIKLIENQTNQVYTSKRNGIFKKAQELTVLDCAKVSLMLSNNTNKHHEYISPTT 62
DB 1 RGKIQIKRIENQTNQVYTSKRNGIFKKAQELTVLDCAKVSLMLSNNTNKHHEYISPTT 60

QY 63 TTKSMYDDYOKTGMGIDLWRTHES 85
DB 61 TTKIEVDLYQTISDVDAATQYE 83

RESULT 5
US-08-867-087B-15
; Sequence 15, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan, E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
US-08-867-087B-15

Query Match 24.3%; Score 295; DB 2; Length 249;
Best Local Similarity 33.1%; Pred. No. 4.2e-21;
Matches 83; Conservative 41; Mismatches 71; Indels 56; Gaps 9;

QY 1 MARGKIEIKLIENQTNQVYTSKRNGIFKKAQELTVLDCAKVSLMLSNNTNKHHEYISPTT 60
DB 1 MGRGRVELKRIENKINQVTFKRRNGLLKAYELSVLDCDAEVALIIFSNRGLKLEFCST 60

QY 61 TTTTKSMYDDYOKTGMGIDLWRTHES-----MKDTLWKLKEINNKLRREIRORLGHDL 113
DB 61 QSMTKTL-EKQKCSYAGPETAQVQRESEQLKASRNEYLKARVENLQRTQRLNGPDL 119

QY 114 NCLSPDELASLDDEMOSSDAIR-----ORKYHVIKTQTTTKKKVKNLEQ 159

DB 120 DSLGKTELESLEKQLDSSLKHVTRTRTKHLVDQLTELQKQCMYSEANRCLRKLSESNH 179

QY 160 REGNN-----LHG-----YFQDEAAGBDP-QYGY--EDNEDGYESA 192

DB 180 VRGQQVWEQGCNLIQYERQPEVQQPLHGGNGFFHPLDAAAGEPTLQIGYPAEHHE----- 233

QY 193 LALSNGANNLY 203
DB 234 -AMNSACMNTY 243

RESULT 6
US-08-867-087B-11
; Sequence 11, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESSEE: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan, E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
US-08-867-087B-11

Query Match 23.8%; Score 290; DB 2; Length 241;
Best Local Similarity 36.7%; Pred. No. 1.2e-20;
Matches 77; Conservative 34; Mismatches 69; Indels 30; Gaps 6;

QY 1 MARGKIEIKLIENQTNQVYTSKRNGIFKKAQELTVLDCAKVSLMLSNNTNKHHEYISPTT 60
DB 1 MGRGRVELKRIENKINQVTFKRRNGLLKAYELSVLDCDAEVALIIFSNRGLKLEFCSS 60

QY 61 TTTTSMYDDYOK-----TMGIDLWRTHEESKMDTLWKLEIKNNKLREIRORLGHDLN 114
Db 61 SSWLKIL-ERYQKNGYAPETNISTREALEISSQOEYKLEKARYEALORSORNLGDLG 119
QY 115 GLSPDELASLDDMOSSLDAR-----QRKYHVKTQTETTTKKVKNLEQR 160
Db 120 PLNSKELESRLQDMSLKIRSTRQTLMDQLDQLDRKEHALNEANTLQRL-----M 174
QY 161 RGNMLHGYFDOEAAGEDPOQGYE--DNEG 188
Db 175 EGSQLNLOWQNA--ODMGYGRQTQTQGD 202

RESULT 7

US-08-867-087B-17
; Sequence 17, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klariquist Sparkman Campbell Leigh &
; ADDRESS: Whinston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204

COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan. E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
US-08-867-087B-17

Query Match 23.6%; Score 287; DB 2; Length 248;
Best Local Similarity 37.7%; Pred. No. 2.5e-20;
Matches 75; Conservative 35; Mismatches 69; Indels 20; Gaps 6;
QY 1 MARGKIEIKLIENQTRQVTSKRRNGIFKKAQELTVLCAKVSIMLNTNKGHEIYSP 60
Db 1 MGRGRVELKRIENKINQVTFKRRNGLLKAYELSVLCAEVALIIFSNRGLYEFCSG 60
QY 61 TTTTSMYDDYOKTM--GIDLWRTHEE-----SMKDTLWKLEIKNNKLREIRORLGHDL 113
Db 61 QSMTRL-ERYQKFSYGGPDTAQNKENELVSSSNEYKLEKARYENLQRTORNLLGDL 119
QY 114 NGLSPDELASLDDMOSSLDARQ-RKYHVKTQTETTTKKVKNLEQR-----GNM 164

Db 120 GTLGIKELEQLKQDSSLRHIRSTQTMQLDQLDQRRREQMCEANKCLARKLESNQ 179
QY 165 LHGYFDOEAAGEDPOQGYE 183
Db 180 LHQOVWEHGA---TLGGE 195

RESULT 8

US-09-611-659A-4
; Sequence 4, Application US/09611659A
; Patent No. 6514760
; GENERAL INFORMATION:
; APPLICANT: Mao, Long
; TITLE OF INVENTION: Jointless Gene of Tomato
; FILE REFERENCE: C218 1010
; CURRENT APPLICATION NUMBER: US/09/611,659A
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-09-611-659A-4

Query Match 23.4%; Score 285; DB 4; Length 265;
Best Local Similarity 31.7%; Pred. No. 4.4e-20;
Matches 73; Conservative 50; Mismatches 69; Indels 38; Gaps 7;

QY 1 MARGKIEIKLIENQTRQVTSKRRNGIFKKAQELTVLCAKVSIMLNTNKGHEIYSP 60
Db 1 MAREKIQIKKIDNSTARQVTFKRRRGLFKAEELSVLCAEVALIIFSTGKLFY--- 57
QY 61 TTTTSMYDDYOKTMGIDLWRTHEESKMDTLWKL-----KEINNKLRREIROR 108
Db 58 ---SSSMKQILERR---DLHKNLEKLDQPSLEQLVENSYSRLSKSEKSHR-LRQM 111
QY 109 LGHDLNGLSPDELASLDDMOSSLDARQK-----YHVKTQTETTTKKX 153
Db 112 RGEELQGLNIEELQQLERSLETGLSRVIERKDXIMREINQLQOKGMHLE-ENEKLRQ 170
QY 154 VKNLEQRRGNMLHGYFDOEAAGEDPOQGYEDNEG-DYESALALSNGANL 202
Db 171 VMEISNNNNNNNGYRAGVVIPEFNGFNNDNQSSSVTNPCNSI 220

RESULT 9

US-09-067-800-2
; Sequence 2, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,800
; FILING DATE:

```

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-067-800-2

Query Match      23.0%; Score 280; DB 3; Length 242;
Best Local Similarity 30.3%; Pred. No. 1.2e-19;
Matches 72; Conservative 48; Mismatches 80; Indels 38; Gaps 7;

QY 1 MARGKIEIKLIENQTNROVTSYKRRNGIFPKKAQELTVLCAKVSLLIMLNTNKKHHEYISP 60
DB 1 MGRGRVQLKRIENKINRQVTSKRRSGLLKKAAHEISVLCDAEVALIVFSSKGLFEYSTD 60
QY 61 TTTTKSM--YDDY---QKTMGIDLWRTHESKMDTLWKLKEINNKLRREI-----RQRL 109
DB 61 SCMERILERYDRLYSDKQLVGRDVSQSEN-----WVLEHAKLKARVEVLEKKNRNF 113
QY 110 GHDLNGLSPDELASLDDEMOSSLDAIRQKYHVIKTQTTTCKKVKVLEQRGNMHLGYF 169
DB 114 GEDLDSLSLKEQLSLEHQLDAIRKSRKQKQAMFESISALQKKDKALQDHNLSLLKKIK 173
QY 170 DOE--AAGED-----POGYEDNEGDEYESALNSGANNLYTFHLHPN 211
DB 174 EREKKTQOEGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGGGASSLT-----EPN 227

; RESULT 10
; US-09-105-652-2
; Sequence 2, Application US/09105652
; Patent No. 6229068
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Martienssen, Robert
; APPLICANT: Ferrandiz, Cristina
; APPLICANT: Gu, Qing
; TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant
; FILE REFERENCE: P-UD 3040
; CURRENT APPLICATION NUMBER: US/09/105,652
; EARLIER FILING DATE: 1998-06-26
; EARLIER FILING DATE: 1997-06-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
; US-09-105-652-2

Query Match      23.0%; Score 280; DB 3; Length 242;
Best Local Similarity 30.3%; Pred. No. 1.2e-19;
Matches 72; Conservative 48; Mismatches 80; Indels 38; Gaps 7;

QY 1 MARGKIEIKLIENQTNROVTSYKRRNGIFPKKAQELTVLCAKVSLLIMLNTNKKHHEYISP 60
DB 1 MGRGRVQLKRIENKINRQVTSKRRSGLLKKAAHEISVLCDAEVALIVFSSKGLFEYSTD 60
QY 61 TTTTKSM--YDDY---QKTMGIDLWRTHESKMDTLWKLKEINNKLRREI-----RQRL 109
DB 61 SCMERILERYDRLYSDKQLVGRDVSQSEN-----WVLEHAKLKARVEVLEKKNRNF 113
QY 110 GHDLNGLSPDELASLDDEMOSSLDAIRQKYHVIKTQTTTCKKVKVLEQRGNMHLGYF 169
DB 114 GEDLDSLSLKEQLSLEHQLDAIRKSRKQKQAMFESISALQKKDKALQDHNLSLLKKIK 173
QY 170 DOE--AAGED-----POGYEDNEGDEYESALNSGANNLYTFHLHPN 211
DB 174 EREKKTQOEGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGGGASSLT-----EPN 227

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-067-800-2

Query Match      23.0%; Score 280; DB 3; Length 242;
Best Local Similarity 30.3%; Pred. No. 1.2e-19;
Matches 72; Conservative 48; Mismatches 80; Indels 38; Gaps 7;

QY 1 MARGKIEIKLIENQTNROVTSYKRRNGIFPKKAQELTVLCAKVSLLIMLNTNKKHHEYISP 60
DB 1 MGRGRVQLKRIENKINRQVTSKRRSGLLKKAAHEISVLCDAEVALIVFSSKGLFEYSTD 60
QY 61 TTTTKSM--YDDY---QKTMGIDLWRTHESKMDTLWKLKEINNKLRREI-----RQRL 109
DB 61 SCMERILERYDRLYSDKQLVGRDVSQSEN-----WVLEHAKLKARVEVLEKKNRNF 113
QY 110 GHDLNGLSPDELASLDDEMOSSLDAIRQKYHVIKTQTTTCKKVKVLEQRGNMHLGYF 169
DB 114 GEDLDSLSLKEQLSLEHQLDAIRKSRKQKQAMFESISALQKKDKALQDHNLSLLKKIK 173
QY 170 DOE--AAGED-----POGYEDNEGDEYESALNSGANNLYTFHLHPN 211
DB 174 EREKKTQOEGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGGGASSLT-----EPN 227
```

```

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-349-677-2

Query Match      23.0%; Score 280; DB 3; Length 242;
Best Local Similarity 30.3%; Pred. No. 1.2e-19;
Matches 72; Conservative 48; Mismatches 80; Indels 38; Gaps 7;

QY 1 MARGKIEIKLIENQTNROVTSYKRRNGIFPKKAQELTVLCAKVSLLIMLNTNKKHHEYISP 60
DB 1 MGRGRVQLKRIENKINRQVTSKRRSGLLKKAAHEISVLCDAEVALIVFSSKGLFEYSTD 60
QY 61 TTTTKSM--YDDY---QKTMGIDLWRTHESKMDTLWKLKEINNKLRREI-----RQRL 109
DB 61 SCMERILERYDRLYSDKQLVGRDVSQSEN-----WVLEHAKLKARVEVLEKKNRNF 113
QY 110 GHDLNGLSPDELASLDDEMOSSLDAIRQKYHVIKTQTTTCKKVKVLEQRGNMHLGYF 169
DB 114 GEDLDSLSLKEQLSLEHQLDAIRKSRKQKQAMFESISALQKKDKALQDHNLSLLKKIK 173
QY 170 DOE--AAGED-----POGYEDNEGDEYESALNSGANNLYTFHLHPN 211
DB 174 EREKKTQOEGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGGGASSLT-----EPN 227

; RESULT 11
; US-09-349-677-2
; Sequence 2, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,800
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-349-677-2

Query Match      23.0%; Score 280; DB 3; Length 242;
Best Local Similarity 30.3%; Pred. No. 1.2e-19;
Matches 72; Conservative 48; Mismatches 80; Indels 38; Gaps 7;

QY 1 MARGKIEIKLIENQTNROVTSYKRRNGIFPKKAQELTVLCAKVSLLIMLNTNKKHHEYISP 60
DB 1 MGRGRVQLKRIENKINRQVTSKRRSGLLKKAAHEISVLCDAEVALIVFSSKGLFEYSTD 60
QY 61 TTTTKSM--YDDY---QKTMGIDLWRTHESKMDTLWKLKEINNKLRREI-----RQRL 109
DB 61 SCMERILERYDRLYSDKQLVGRDVSQSEN-----WVLEHAKLKARVEVLEKKNRNF 113
QY 110 GHDLNGLSPDELASLDDEMOSSLDAIRQKYHVIKTQTTTCKKVKVLEQRGNMHLGYF 169
DB 114 GEDLDSLSLKEQLSLEHQLDAIRKSRKQKQAMFESISALQKKDKALQDHNLSLLKKIK 173
QY 170 DOE--AAGED-----POGYEDNEGDEYESALNSGANNLYTFHLHPN 211
DB 174 EREKKTQOEGQLVQCSNSSSVLLPQYCVTSSRDGFVERVGGGASSLT-----EPN 227
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RESULT 12
US-09-708-584-2
; Sequence 2, Application US/09708584
; Patent No. 6541683
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Martienssen, Robert
; APPLICANT: Ferrandiz, Cristina
; APPLICANT: Gu, Qing
; TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant
; FILE REFERENCE: P-UD 3040
; CURRENT APPLICATION NUMBER: US/09/708,584
; CURRENT FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/105,652
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/051,030
; PRIOR FILING DATE: 1997-06-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-708-584-2

Query Match 23.0%; Score 280; DB 4; Length 242;
Best Local Similarity 30.3%; Pred. No. 1.2e-19;
Matches 72; Conservative 48; Mismatches 80; Indels 38; Gaps 7;
QY 1 MARGKIEIKLIENQNRQVTSYKRRNGIFPKAQLTVLCAKVSIMLNTNKGHEYISP 60
DB 1 MGRGRVQLKRIENKINRQVTSYKRRNGIFPKAQLTVLCAKVSIMLNTNKGHEYISP 60
QY 61 TTTTSM--YDDY---QKTGIDLWRTHESKMDTLWKLKEINNKLRRI-----RQL 109
DB 61 SCWERILERYDLYSDQLQVDRVDSQEN-----WVLEHAKLKARVEVLEKNKRNF 113
QY 110 GHLNGLSFLDELASLDDMQSSLDARQKHYVIKTQTETTTKKVQKLEQRRGNMLHGYF 169
DB 114 GEDLSLSLKLQSLQSLHQLDAIKRSIRKQAMFESISALQKDKALQDHNNLSLKKIK 173
QY 170 DOE-AAGED-----POGYENEGDYESALALSNGCANLYTFHLHPN 211
DB 174 EREKKTGQEGQLVOCSSNVLLPQVCVTSRDFVVRVGGNGGASLT-----EPN 227

RESULT 13
US-09-067-800-8
; Sequence 8, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/067,800
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2948
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLESCALE TYPE: protein
US-09-067-800-8

Query Match 22.9%; Score 279; DB 3; Length 246;
Best Local Similarity 30.6%; Pred. No. 1.5e-19;
Matches 74; Conservative 40; Mismatches 72; Indels 56; Gaps 6;
QY 1 MARGKIEIKLIENQNRQVTSYKRRNGIFPKAQLTVLCAKVSIMLNTNKGHEY--- 57
DB 16 IGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCAEVALVIFSTRGLRLEYANN 75
QY 58 -----ISPTTTTKSMYDDYQKTMGIDLWRTHESKMDTLWKLKEINNK 101
DB 76 SVRGTIERYKKACSDAVNPPTITEANTQYYQEA-----SKL 112
QY 102 RREI-----RQLGHLNGLSFLDELASLDDMQSSLDARQKHYVIKTQTETTKKV 154
DB 113 RRQRDIQNLRNHLGSLGSLNFKELKNLESLEKGISRVRSKKHEMLVABEYMQK-- 170
QY 155 KNLSORGNMLHGYFDOEAAGEDPOGYENEGD-YESALALSNGA-----NNLYTFHLHH 209
DB 171 REILQNDNMYLASKITERITGLQQQSSVHQTIVYESGVTSSHQSGQNRNYIANVLL 230
QY 210 PN 211
DB 231 PN 232

RESULT 14
US-09-349-677-8
; Sequence 8, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/349,677
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,800
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-349-677-8
Query Match 22.9%; Score 279; DB 3; Length 246;
Best Local Similarity 30.6%; Pred. No. 1.5e-19;
Matches 74; Conservative 40; Mismatches 72; Indels 56; Gaps 6;
QY 1 MARGKIEIKLIENQTNQVTSKRRNGIFKKAQELTVLCDKAVSLMLSLNTNKHHEYIS 57
Db 16 IGRGKIEIKRIENTTNQVTFCKRNGLLKAYELSVLCAEVALVIFSTRGLYEYANN 75
QY 58 -----ISPTTTKSMYDDYQKTMGIDLWRTHESMDTLWLKKEINNK 101
Db 76 SVRGTIERYKKACSDAVNPFTITANTQYQEA-----SKL 112
QY 102 RREI-----RQLGHDNLGLSFDLASLDDMOSSLDAIRQRYHVIKTQTETTKKV 154
Db 113 RRQIRDIQNLNRHILGESLGNFKELKNLESRLKGISRVRSKKHEMLVAEIEYMQ-- 170
QY 155 KNLQRRCNMLHGYFDQEAAGEDPQGYEDNEG-YESALALSNGA-----NNLYTEHLH 209
Db 171 REIELQNDNMYLRSKITERTGLQQQESSVHGGTVYESGVTSSHQSGQYNNYIANVLE 230
QY 210 PN 211
Db 231 PN 232

RESULT 15
US-08-904-284-7
Sequence 7, Application US/08904284
Patent No. 6133435
GENERAL INFORMATION:
APPLICANT: Fernandez, Donna E.
APPLICANT: Heck, Gregory R.
TITLE OF INVENTION: EXPRESSION OF AGL15 SEQUENCE IN
TITLE OF INVENTION: TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Finckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,284
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.94193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-904-284-7
Query Match 22.7%; Score 276; DB 3; Length 268;
Best Local Similarity 40.0%; Pred. No. 3.4e-19;
Matches 68; Conservative 33; Mismatches 41; Indels 28; Gaps 5;
QY 1 MARGKIEIKLIENQTNQVTSKRRNGIFKKAQELTVLCDKAVSLMLSLNTNKHHEYIS 60
Db 1 MGRGKIEIKRIENANSRQVTFKRRSGLKKARELSVLCDAEVAVIVFSKSKLFEYST 60
QY 61 -TTTTKSMYDDYQKTMG-----IDLWRTHESMDTLWLKKEINNKLRREIRQLG 110
Db 61 GMKQTLRSRYGNHQSASSAKAEEDCAEVDI-----LKDQLSKLQEKHLQLQ-----G 106
QY 111 HDINGLSPDELASLDDMOSSLDAIRQRYHVIKTQTETTKKVKVKNLEOR 160
Db 107 KGLNPLTFKELQSLQQLYHALITVRERKERLLTNQLEESRLK-----EOR 152
Search completed: September 27, 2004, 09:30:03
Job time : 24.8747 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 09:22:14 ; Search time 22.1253 Seconds
(without alignments)
501.670 Million cell updates/sec

Title: US-10-069-527-2

Perfect score: 1103

Sequence: 1 MGRGKVEIKRINSNRQVT.....QQIPFAFRVQPIQPNLQERI 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	358	32.5	227	4	US-09-410-464-4
2	346	31.4	273	2	US-08-592-214A-8
3	346	31.4	273	3	US-08-659-188-8
4	346	31.4	273	3	US-08-655-227-8
5	346	31.4	273	3	US-08-655-241-8
6	346	31.4	273	3	US-09-149-976-8
7	346	31.4	273	4	US-09-398-326-8
8	334	30.3	265	4	US-09-611-659A-4
9	330	29.9	242	3	US-09-067-800-2
10	330	29.9	242	3	US-09-105-652-2
11	330	29.9	242	3	US-09-349-677-2
12	330	29.9	242	4	US-09-708-584-2
13	321	29.1	255	2	US-08-592-214A-10
14	321	29.1	255	3	US-08-659-188-10
15	321	29.1	255	3	US-08-655-227-10
16	321	29.1	255	3	US-08-655-241-10
17	321	29.1	255	3	US-09-149-976-10
18	321	29.1	255	4	US-09-398-326-10
19	320.5	29.1	248	3	US-09-067-800-6
20	320.5	29.1	248	3	US-09-349-677-6
21	319.5	29.0	246	3	US-09-067-800-8
22	319.5	29.0	246	3	US-09-349-677-8
23	319	28.9	252	1	US-08-460-512-5
24	319	28.9	252	2	US-08-592-214A-6
25	319	28.9	255	3	US-08-659-188-6
26	319	28.9	255	3	US-08-655-227-6
27	319	28.9	255	3	US-08-655-241-6

28	319	28.9	255	3	US-09-149-976-6	Sequence 6, Appli
29	319	28.9	255	4	US-09-398-326-6	Sequence 6, Appli
30	319	28.9	285	1	US-08-460-512-2	Sequence 2, Appli
31	318	28.8	253	2	US-08-592-214A-4	Sequence 4, Appli
32	318	28.8	253	3	US-08-659-188-4	Sequence 4, Appli
33	318	28.8	253	3	US-08-655-227-4	Sequence 4, Appli
34	318	28.8	253	3	US-08-655-241-4	Sequence 4, Appli
35	318	28.8	253	4	US-09-149-976-4	Sequence 4, Appli
36	318	28.8	253	4	US-09-398-326-4	Sequence 4, Appli
37	318	28.8	255	2	US-08-576-156-2	Sequence 2, Appli
38	318	28.8	256	3	US-08-653-188-2	Sequence 2, Appli
39	318	28.8	256	3	US-08-655-227-2	Sequence 2, Appli
40	318	28.8	256	3	US-08-655-241-2	Sequence 2, Appli
41	318	28.8	256	4	US-09-398-326-2	Sequence 2, Appli
42	318	28.8	300	2	US-08-592-214A-2	Sequence 2, Appli
43	318	28.8	300	3	US-09-149-976-2	Sequence 2, Appli
44	315.5	28.6	241	3	US-08-867-087B-11	Sequence 11, Appli
45	314.5	28.5	251	2	US-08-592-214A-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1

US-09-410-464-4

; Sequence 4, Application US/09410464

; Patent No. 6395892

; GENERAL INFORMATION:

; APPLICANT: Strauss et al.

; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in poplar and other plant species.

; FILE REFERENCE: 53375

; CURRENT APPLICATION NUMBER: US/09/410,464

; CURRENT FILING DATE: 1999-10-01

; EARLIER APPLICATION NUMBER: 09/287,700

; EARLIER FILING DATE: 1999-04-06

; EARLIER APPLICATION NUMBER: 60/080,851

; EARLIER FILING DATE: 1998-04-06

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 227

; TYPE: PRT

; ORGANISM: Populus balsamifera subsp. trichocarpa

; US-09-410-464-4

Query Match	32.5%;	Score 358;	DB 4;	Length 227;
Best Local Similarity	35.6%;	Pred. No. 3.9e-26;		
Matches	79;	Conservative 39;	Mismatches 64;	Indels 40;
Gaps	3;			
Qy	1	MGRGKVEIKRINSNRQVTYSKRRNGITLKAKETVLCDKAVSLIYSSSGRWVEYCSF	60	
Db	1	MGRGKIEIKKIENPTNRQVTYSKRRNGIFKKAQELIVLCDKAVSLIMFNTKLNKYISF	60	
Qy	61	STLTILDKYHSGSKLWDKAKHNLSEVDRVKDNDMSQVHLRHLKGEDITSLNHVE	120	
Db	61	STSTKKIYQYQNALGIDLWGTYEKWQEHRLKRLNDINHLKQRIQRGRGGLNLSIDH	120	
Qy	121	LMALEALENGLTSIRDKSKFVDMWRDNGKALEDENKELTYELQCKQEMKIKENVNME	180	
Db	121	LRLEQHMTEALNGVGRK-----YHVIKTQNETRYKKVKNLE	158	
Qy	181	NGV-----HORQLGNVNN-----NOQIIPFAFRV	204	
Db	159	ERHGNLLMEYAEKLEDRQYGLVDNEAAVALANGASNLVAFRL	200	

RESULT 2

US-08-592-214A-8

; Sequence 8, Application US/08592214A

; Patent No. 5811536

; GENERAL INFORMATION:

; APPLICANT: Yanofsky, Martin F.

Query Match	31.4%;	Score 346;	DB 3;	Length 273;
Best Local Similarity	36.7%;	Pred. No. 6.9e-25;		

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Query Match      31.4%; Score 346; DB 3; Length 273;
Best Local Similarity 36.7%; Pred. No. 6.9e-25;
Matches 83; Conservative 51; Mismatches 58; Indels 34; Gaps 7

QY      1 MGRGKVEIKR1ENGNSRQVTVYSKRNIGIIKKAEITVLCDAKVSLIIYSSSGKMYEYCSP 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db       1 MGRGK1VQLKRIENKINQVTFSKRNLGLLKAHEISVLCDAEVAVIVFSPKGLIYEIYND 60

QY      61 STLTLEILDKY1-HQSGKKLWDAKHE--NLSNEYDVRKNDNSQVRELRLHKGEDITS 115
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db       61 S-RMDKILERYERYSAEKALISAESSEGNWCHYEYRKLKAKIETITQCKHKLMGEDLES 119

QY      116 LNHVELMALEALENGITSTIRDKQS--KFDVMDNDNGKALEDENKRLTYEL----- 164
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db       120 LNPKELOQLBOQLDSSLKHIRSKSHLMAESISELQCKERSLQEEVKALQKELAEKRAQKAV 179

QY      165 ---QKQEMKI-----KENVRNMENGYHQ1QQLGNYNNNQQIIP 199
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db       180 ASRQCCQCCQCCQVWDQOOTHQAQAT1SSSSSSPFMSQ-----DOGLP 219

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RESULT 4
US-08-655-227-8
; Sequence 8, Application US/08655227
; Patent No. 6025483
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Maize and Cauliflower APTALAL Gene
; ; Products and Nucleic Acid Molecules Encoding Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,227
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/POCKET NUMBER: P-UD 2143
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-655-241-8

Query Match 31.4%; Score 346; DB 3; Length 273;
Best Local Similarity 36.7%; Pred. No. 6.9e-25;
Matches 83; Conservative 51; Mismatches 58; Indels 34; Gaps 7;

QY 1 MGRGKVEIKRIENSSNRQVTSKRRNGIISKAKEITVLCDKAVSLIIYSSSGKQVVEYCSF 60
DB 1 MGRGKVLKRIENKINRQVTSKRRNGLLKKAHEISVLCDAEAVIVFSPKGLYEYATD 60
QY 61 STTLTEILDY--HGQSGKKLWDKHE---NLSNEVDVRVKDNDMSQVLRHLKGEDITS 115
DB 61 S-RMDKILERYERYSAEKALISAESSEGNWCHEYKRLKAKIETIQCKHKLMDGEDLES 119
QY 116 LNHVLMALAEALENGTSIRDQS---KFVDMMRDNGKALEDENKRLTYEL----- 164
DB 120 LNPKEQLQLEQDSSLKHSRSHLMAESISELQKERSLQENKALQKELAEQKAV 179
QY 165 ---QKQEMKI-----KENVRNMENGVHQRLGNYNNOQIIP 199
DB 180 ASRQQQQQQVQWQDQTHAQATSSSSSFMFRQ-----DQGLP 219

RESULT 5
US-08-655-241-8
; Sequence 8, Application US/08655241
; Patent No. 6025543
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Weigel, Detlef
; TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
; TITLE OF INVENTION: Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: CLASS 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1894
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-655-241-8

Query Match 31.4%; Score 346; DB 3; Length 273;
Best Local Similarity 36.7%; Pred. No. 6.9e-25;
Matches 83; Conservative 51; Mismatches 58; Indels 34; Gaps 7;

QY 1 MGRGKVEIKRIENSSNRQVTSKRRNGIISKAKEITVLCDKAVSLIIYSSSGKQVVEYCSF 60
DB 1 MGRGKVLKRIENKINRQVTSKRRNGLLKKAHEISVLCDAEAVIVFSPKGLYEYATD 60
QY 61 STTLTEILDY--HGQSGKKLWDKHE---NLSNEVDVRVKDNDMSQVLRHLKGEDITS 115
DB 61 S-RMDKILERYERYSAEKALISAESSEGNWCHEYKRLKAKIETIQCKHKLMDGEDLES 119
QY 116 LNHVLMALAEALENGTSIRDQS---KFVDMMRDNGKALEDENKRLTYEL----- 164
DB 120 LNPKEQLQLEQDSSLKHSRSHLMAESISELQKERSLQENKALQKELAEQKAV 179
QY 165 ---QKQEMKI-----KENVRNMENGVHQRLGNYNNOQIIP 199
DB 180 ASRQQQQQQVQWQDQTHAQATSSSSSFMFRQ-----DQGLP 219

RESULT 6
US-09-149-976-8
; Sequence 8, Application US/09149976
; Patent No. 6127123
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identity
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 09-SEP-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,214
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 3291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-149-976-8

Query Match 31.4%; Score 346; DB 3; Length 273;
Best Local Similarity 36.7%; Pred. No. 6.9e-25;
Matches 83; Conservative 51; Mismatches 58; Indels 34; Gaps 7;

QY 1 MGRGKVEIKRIENSSNRQVTSKRRNGIISKAKEITVLCDKAVSLIIYSSSGKQVVEYCSF 60
DB 1 MGRGKVLKRIENKINRQVTSKRRNGLLKKAHEISVLCDAEAVIVFSPKGLYEYATD 60
QY 61 STTLTEILDY--HGQSGKKLWDKHE---NLSNEVDVRVKDNDMSQVLRHLKGEDITS 115
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Db 61 S-RMDKILERYERYSAEKALISAESSEGNWCHYRKLKAKIETIQCKHLMGEDLES 119
QY 116 LNHVELMALEALENGLTSTDKOS----KFVDMRDNGKALDENKRLTYEL----- 164
Db 120 LNPKELOQEQLOSLKHIRSKRSHLMAESISELQCKERSLOENKALQKELAERQKAV 179
QY 165 ---KQCKEMKI-----KENVRNMENGYHORQLGNYNNOQQIP 199
Db 180 ASRQOQQOQQVQWQDQTHAQATSSSSSFFMRQ-----DQOGLP 219

RESULT 7
US-09-398-326-8
; Sequence 8, Application US/09398326
; Patent No. 6355863
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; TITLE OF INVENTION: Reproductive Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/398,326
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/659,188
; FILING DATE: 05-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 3739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-398-326-8

Query Match 31.4%; Score 346; DB 4; Length 273;
Best Local Similarity 36.7%; Pred. No. 6.9e-25;
Matches 83; Conservative 51; Mismatches 58; Indels 34; Gaps 7;

QY 1 MGRGKVEIKRIENSNRQVTYSKRRNGIIRKAKEITVLCDAKVSIIYSSSGKMYEYCSP 60
Db 1 MGRGKVLKRIENKINRQVTFSKRRGLKKAHESVLCDAEAVIVFSPKGLKYEYATD 60
QY 61 STTLTEILDY--HGOSGKKLWDKHE---NLSNEVDYRVKNDNSMQVELRHLKGEDITS 115
Db 61 S-RMDKILERYERYSAEKALISAESSEGNWCHYRKLKAKIETIQCKHLMGEDLES 119
QY 116 LNHVELMALEALENGLTSTDKOS----KFVDMRDNGKALDENKRLTYEL----- 164
Db 120 LNPKELOQEQLOSLKHIRSKRSHLMAESISELQCKERSLOENKALQKELAERQKAV 179
QY 165 ---KQCKEMKI-----KENVRNMENGYHORQLGNYNNOQQIP 199
Db 180 ASRQOQQOQQVQWQDQTHAQATSSSSSFFMRQ-----DQOGLP 219

RESULT 8
US-09-611-659A-4
; Sequence 4, Application US/09611659A
; Patent No. 6514760
; GENERAL INFORMATION:
; APPLICANT: Mao, Long
; APPLICANT: Rod, Wing
; TITLE OF INVENTION: Jointless Gene of Tomato
; FILE REFERENCE: C218 1010
; CURRENT APPLICATION NUMBER: US/09/611.659A
; CURRENT FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-09-611-659A-4

Query Match 30.3%; Score 334; DB 4; Length 265;
Best Local Similarity 38.1%; Pred. No. 9e-24;
Matches 82; Conservative 45; Mismatches 58; Indels 30; Gaps 8;

QY 1 MGRGKVEIKRIENSNRQVTYSKRRNGIIRKAKEITVLCDAKVSIIYSSSGKMYEYCSP 60
Db 1 MAREKIQIKKIDNSTARQVTFKRRGLFKKABELSVLCDAVALIIFSTGKLFYSSS 60
QY 61 STTLTEILDY--YHGOSGKKLWDKHE---SNEVDYRVKNDNSMQVELRHLKGEDIT 114
Db 61 S--MKQILERRDLHSHKNLEK--DQPSLEQLQVENSYSRLSKSEKSHLQKRGSEELQ 117
QY 115 LNHVELMALEALENGLTST---RDQSKFVDMRDNGKALDENKRLTYELQKQEM 170
Db 118 GLNTEELQQLERSLETGSRVIERKDGKIMREINQLOQKGMHLMEENKL-----RQOVM 172
QY 171 KIKENVRNMENGYHORQLG-----NYYNNQ 195
Db 173 EISNNNNNNNGY--REAGVIFEPENGFNNNNE 205

RESULT 9
US-09-067-800-2
; Sequence 2, Application US/09067800
; Patent No. 6198024
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,800
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2948
; TELECOMMUNICATION INFORMATION:

```

RESULT.11:
US-09-349-677-2
; Sequence 2, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed plants Characterized by Delayed
; TITLE OF INVENTION: Seed Dispersal
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,677
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/067,800

```

ATTORNEY/AGENT INFORMATION:
NAME: Cambell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: F-UD 2948
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

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QY 61 STTLTEILDKY--HQOSKKI-----WAKHENISNEVDVRVKKONDSMOVELRHL 100
Db 60 DSCMERILLERYDRLVYSKQLVGRDVSQSENWVLEHAUKARVEVLEKXK-----RNF 112
QY 109 KGEEDITSNHVELMALEAEALNGTSLTDRKQS---KFDMMRDNGKALDEENKRLTYEL 164
Db 113 MEEDLDSLSLKEQLQSLHQLEHDAAIKTSRSRKQAMFESISALQKDKALQDHNSLL--- 169
QY 165 QKQEMKIKENVRNMYGHOBLGNTYNNNQOQIPFAFRVQPTQPNLQSR 215
Db 170 -----KKIKE--REKTKQEQGLVQCSNSSVLLPQYCVTSRRDGFVERV 213

RESULT 12
US-09-708-584-2
; Sequence 2, Application US/09708584
; Patent No. 6541683
; GENERAL INFORMATION:
; APPLICANT: Yancofsky, Martin F.

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RESULT 12
US-09-708-584-2
; Sequence 2, Application US/09708584
; Patent No. 6541683
; GENERAL INFORMATION:
; APPLICANT: Yano,fsky, Martin F.

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; APPLICANT: Martienssen, Robert
; APPLICANT: Ferrandiz, Crisina
; APPLICANT: Gu, Qing
; TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant
; FILE REFERENCE: P-UD 3040
; CURRENT APPLICATION NUMBER: US/09/708,584
; CURRENT FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 09/105,652
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/051,030
; PRIOR FILING DATE: 1997-06-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
; US-09-708-584-2

Query Match          29.9%; Score 330; DB 4; Length 242;
Best Local Similarity 35.9%; Pred. No. 1.9e-23;
Matches 83; Conservative 46; Mismatches 68; Indels 34; Gaps 7;

QY 1 MGRGKVEIKRIENSSNRQVTSYKRNGLIHKAKETVLCDAKVSLIYSSSGKQWVEYCSP 60
DB 1 MGRGVQLKRIENKINRQVTSFKRRSGLLKAHEISVLCDAEVALIVFSSKGLPEY-ST 59
QY 61 STLTTEILDKYK- -HGQSGKKL- - - - -WDAKHENLSNEVDVRYKKDNDMSQVELRHL 108
DB 60 DSCMERILERYDLYSLDKQLVGRDVSQSENWVLEHAKUKARVEVLEKNK- - - - -RNF 112
QY 109 KGEDITSLSNHELMALFEALENGLSITSIRDKQS- - - - -KFVDMRDNGKALEDENKRLTYEL 164
DB 113 MGEDLSLSLKEQLSLEHQLDAIKSIRSKNQAMFESISALQKDKALQDHNSSL- - - - - 169
QY 165 QKQEMKIKENVRNMGYHQRLGNVNNNQOIPFAFRVQPIQPNLQRI 215
DB 170 - - - - -KKIKE- -REKGTQOQEGQLVQCSNSSVLLPQYCVTSRDFVERV 213

RESULT 13
US-08-592-214A-10
; Sequence 10, Application US/08592214A
; Patent No. 5811536
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Cauliflower Floral Meristem Identify
; TITLE OF INVENTION: Genes and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,214A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1927
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9001
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-708-584-2

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-592-214A-10

Query Match          29.1%; Score 321; DB 2; Length 255;
Best Local Similarity 35.9%; Pred. No. 1.4e-22;
Matches 80; Conservative 49; Mismatches 68; Indels 26; Gaps 8;

QY 1 MGRGKVEIKRIENSSNRQVTSYKRNGLIHKAKETVLCDAKVSLIYSSSGKQWVEYCSP 60
DB 1 MGRGVQLKRIENKINRQVTSFKRRSGLLKAHEISVLCDAEVALIVFSSKGLPEY-SE 60
QY 61 STLTTEILDKYHQS- -GKKLWDK- - - - -ENLSNEVDVRYKKDNDMSQVELRHLKGED 113
DB 61 S-CMEKVLERYVSYAERQLIAPDSHVNAQTNSMEYSLKAKIETLERNQRYLGEEL 119
QY 114 TSLNHELMALFEALENGLSITSIRDKQS- - - - -VDMRDNGKALEDENKRLTYELQKQE 169
DB 120 EPMKLDQLQNLQLEQLETKLXIRSKNQLMNESLNHLQKEKEIQEENSMLT- - - - -KQ 173
QY 170 MKIKENVRNMGYHQRLGNVNNNQOIPFAFRVQPIQ-PNL 211
DB 174 IKERENILKTK- - - - -QTQCEQLNESVDDVP- - - - -QPQFQPHL 209

RESULT 14
US-08-659-188-10
; Sequence 10, Application US/08659188
; Patent No. 6002069
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; TITLE OF INVENTION: Reproductive Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,188
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-659-188-10

Query Match          29.1%; Score 321; DB 3; Length 255;
Best Local Similarity 35.9%; Pred. No. 1.4e-22;
Matches 80; Conservative 49; Mismatches 68; Indels 26; Gaps 8;

QY 1 MGRGKVEIKRIENSSNRQVTSYKRNGLIHKAKETVLCDAKVSLIYSSSGKQWVEYCSP 60

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Mon Sep 27 09:56:01 2004

us-10-069-527-2.ra1

Db 174 IKERENILKTK-----QTQCEQLNRSVDDVP---QPQPFQHPHL 209
Search completed: September 27, 2004, 09:30:02
Job time : 23.1253 secs

Db 1 MGRGRVELKRIENKINQVTSKRTGLLKKAAQETSVLCDAEVSILVFSHGKLFYSS 60
QY 61 STTLTEILDYKHQS---GKKLWDKXH---ENLSNEVDVRYKKONDSMQVELRLKGBDI 113
Db 61 S-CMEKVLERYERYAERQLIAPDSHVAQTNWSEYSLKAKIELLERNQRYLGBEL 119
QY 114 TSLNHVELMALEALENGLTISIRDKSKF---VDMMRDNGKALEDENKRLTYELQKQOE 169
Db 120 EPMSLKDLQNLQEQLETALKHRSRKNQMLNBSLNLHQRKEKEIQEENSMLT-----KQ 173
QY 170 MKIKENVRNMENGYHQRLGNYNNNQOQIPFAFRVQPIQ-PNL 211
Db 174 IKERENILKTK-----QTQCEQLNRSVDDVP---QPQPFQHPHL 209

RESULT 15
US-08-655-227-10
; Sequence 10, Application US/08655227
; Patent No. 6025483
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Maize and Cauliflower APETALAI Gene
; TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,227
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2143
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-655-227-10

Query Match 29.1%; Score 321; DB 3; Length 255;
Best Local Similarity 35.9%; Pred. No. 1.4e-22;
Matches 80; Conservative 49; Mismatches 68; Indels 26; Gaps 8;
QY 1 MGRGRVELKRIENKINQVTSKRTGLLKKAAQETSVLCDAEVSILVFSHGKLFYSS 60
Db 1 MGRGRVELKRIENKINQVTSKRTGLLKKAAQETSVLCDAEVSILVFSHGKLFYSS 60
QY 61 STTLTEILDYKHQS---GKKLWDKXH---ENLSNEVDVRYKKONDSMQVELRLKGBDI 113
Db 61 S-CMEKVLERYERYAERQLIAPDSHVAQTNWSEYSLKAKIELLERNQRYLGBEL 119
QY 114 TSLNHVELMALEALENGLTISIRDKSKF---VDMMRDNGKALEDENKRLTYELQKQOE 169
Db 120 EPMSLKDLQNLQEQLETALKHRSRKNQMLNBSLNLHQRKEKEIQEENSMLT-----KQ 173
QY 170 MKIKENVRNMENGYHQRLGNYNNNQOQIPFAFRVQPIQ-PNL 211

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 09:10:49 ; Search time 85.6152 Seconds
(without alignments)
709.543 Million cell updates/sec

Title: US-10-069-527-2

Perfect score: 1103

Sequence: 1 MGRGKVEIKIENSSNRQVT.....QQIPFAFRVQPIQPNLQERI 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1103	100.0	215	4	AAU00186
2	684.5	62.1	210	2	AA46555 fbp1, for
3	660.5	59.9	208	3	AA821899 Arabidops
4	650	58.9	209	5	ABG60941 Novel flo
5	650	58.9	260	5	ABG60932 Novel flo
6	645	58.5	209	5	ABG60942 Novel flo
7	640	58.0	209	5	ABG60945 Novel flo
8	639.5	58.0	212	3	AA40904 Zea mays
9	623	56.5	209	5	AAE25756 Corn AP3
10	435.5	39.5	155	3	AA821900 Arabidops
11	406.5	36.9	224	5	AAE25763 Rice MADS
12	401.5	36.4	147	3	AA821901 Arabidops
13	398.5	36.1	227	5	AAE25755 Corn AP3
14	377.5	34.2	231	2	AAE43385
15	377	34.2	227	5	AAE25757 Soybean A
16	358.5	32.5	233	3	AB32552 Eucalyptu
17	358	32.5	227	4	AB68435 Amino aci
18	358	32.5	227	5	ABG30865 Poplar pr
19	358	32.5	227	7	ABU61893 Poplar ho
20	357.5	32.4	232	3	AA825577 Arabidops
21	357.5	32.4	242	3	AA825576 Arabidops
22	356.5	32.3	232	3	AA854029 Arabidops
23	356.5	32.3	236	3	AA854679 Arabidops
24	356.5	32.3	241	3	AA854028 Arabidops
25	355.5	32.2	232	4	AAU00187 Granny Sm

26	354	32.1	171	3	AA825218 Arabidops
27	354	32.1	181	3	AA825217 Arabidops
28	353.5	32.0	267	4	AA873250 Rice MADS
29	352	31.9	227	3	AA558654 Poplar PT
30	349.5	31.7	270	4	AA68357 Amino aci
31	346	31.4	273	4	AA23814 Maize flo
32	346	31.4	273	2	AAW69328 Zea mays
33	346	31.4	273	2	AAW43112 APETALA1
34	346	31.4	273	2	AAW43329 Arabidops
35	346	31.4	273	2	AAW39134 Maize flo
36	346	31.4	273	3	AA567553 Zea mays
37	346	31.4	273	3	AA819244 Amino aci
38	346	31.4	273	3	AA78883 Corn APET
39	345.5	31.3	262	3	AA569920 MADS box
40	337	30.6	238	5	AAU92966 Arabidops
41	337	30.6	238	7	ADC46635 Thalecres
42	337	30.6	238	7	ADD30296 Plant yie
43	335.5	30.4	250	3	AA817604 Arabidops
44	335.5	30.4	260	3	AA817603 Arabidops
45	335.5	30.4	269	3	AA84911 Amino aci

ALIGNMENTS

RESULT 1

AAU00186

ID AAU00186 standard; peptide; 215 AA.

XX

AC AAU00186;

XX

DT 11-SEP-2003 (revised)

DT 17-MAY-2001 (first entry)

XX

DE Granny Smith apple MdPI protein.

XX

KW Granny Smith apple; MdPI; seedless fruit; horticulture;

KW accelerated breeding programme; cross pollination; transgenic plant;

KW biennial bearing tendency; codling moth.

XX

OS Malus x domestica; var. Granny Smith.

XX

PN WO200117334-A1.

XX

PD 15-MAR-2001.

XX

PF 07-SEP-2000; 2000WO-NZ000176.

XX

PR 07-SEP-1999; 99NZ-00337688.

XX

PA (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.

XX

PI Yao J, Morris BA;

XX

DR WPI; 2001-235145/24.

XX

N-PSDB; AAS00103.

XX

PT New genetically modified fruiting plants that does not functionally express MdPI or MdAP3 peptides useful for producing seedless fruits, specifically apple and its related species.

XX

PS Claim 1; Fig 2; 4ipp; English.

XX

CC The sequence represents Granny Smith apple MdPI. The invention concerns a fruiting plant that has been genetically modified so that it does not functionally express the MdPI or MdAP3 peptide, producing seedless

CC fruits. The DNA constructs encoding non-functional variants of MdPI/MdAP3 may be used to transform fruiting plants, specifically apple and pear.

CC The polynucleotides may be used in modulating, reducing or eliminating seed-bearing capacity in fruiting plants, used in horticulture, and in breeding programmes to monitor the progress in breeding a stable seedless

CC fruiting plant. The polynucleotides may also be used in programmes for identifying nucleic acid variants from fruiting plants. They can be used

CC for pre-selecting plants (mutated in MdPI, MdAP3 or their equivalents),
 CC for use in an accelerated breeding programme to produce seedless fruit.
 CC They may also be used in designing probes and primers for MdPI or MdAP3,
 CC or their variants. The seedless fruiting plant is more convenient than
 CC seeded fruit since these can be cropped without pollination, reducing
 CC dependence on bees, pollinator varieties and warm weather at flowering.
 CC The absence of pollen is also advantageous to alleviate environmental
 CC concerns regarding the transfer of transgenes to non-transgenic by cross
 CC pollination. Seedless cultivars can also avoid or reduce biennial bearing
 CC tendencies that have been attributed to the inhibition of flower bud
 CC formation by developing seeds and are less susceptible to codling moth
 CC compared to seeded fruit. (Updated on 11-SEP-2003 to standardise OS
 CC field)
 XX
 XX Sequence 215 AA;

Query Match 100.0%; Score 1103; DB 4; Length 215;
 Best Local Similarity 100.0%; Pred. No. 1.2e-87;
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGRGKVEIKRIENSSNQVTSYKRRNGIHKAKEITVLCDAKVSIIYSSGGWVEYCSF 60
 DB 1 MGRGKVEIKRIENSSNQVTSYKRRNGIHKAKEITVLCDAKVSIIYSSGGWVEYCSF 60
 QY 61 STTILTEILDKYHGSQGGKLLWDAKHENLSNEVDVKKNDNSQVLEHLKGEDITSLNHVE 120
 DB 61 STTILTEILDKYHGSQGGKLLWDAKHENLSNEVDVKKNDNSQVLEHLKGEDITSLNHVE 120
 QY 121 LMALEALENGLTSIRDKQSKFVDMRDNGKALEDENKRLTYELOKQOEMKIKENVRNME 180
 DB 121 LMALEALENGLTSIRDKQSKFVDMRDNGKALEDENKRLTYELOKQOEMKIKENVRNME 180
 QY 181 NGYHORLGNVNNQOQIPFAFRVQPIQPNLQERI 215
 DB 181 NGYHORLGNVNNQOQIPFAFRVQPIQPNLQERI 215

RESULT 2
 AAR46555
 ID AAR46555 standard; protein; 210 AA.
 AC AAR46555;

DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 25-JUN-1994 (first entry)

XX fbp1, for reverse genetic techniques.

XX Flower; morphology; petals; MADS box protein; toxin gene; insect;
 XX resistance; Frankliniella occidentals; plant.

XX Petunia x hybrida.

XX WO9400582-A2.

XX 06-JAN-1994.

XX 07-JUN-1993; 93WO-NL000121.

XX 30-JUN-1992; 92EP-00201951.

XX (CPRO-) CPRO-DLO CENT PLANT BREEDING & REPRODUCT.

XX Van Tunen A7, Mollena C, Angenent GC, Dons JUM;

XX WPI; 1994-026218/03.

XX DR N-PSDB; AAR455089.

XX New nucleic acid which alters flower morphology - by suppressing petals
 XX and stamen(s), or converts them to other organs, partic. to produce
 XX transgenic plants less susceptible to insect pests.

PS Disclosure; Fig 1A; 33pp; English.

XX A flower specific gene fbp1 was isolated from the genome of Petunia
 CC hybrida. This gene has the features of a transcription factor and belongs
 CC to the group of MADS box genes. The fbp1 gene is only active during
 CC differentiation of floral organ primordia and plays a crucial role in the
 CC determination of part of the floral meristem into petals and stamen
 CC primordia. Plants transformed with the gene are less attractive to insect
 CC pests so have better resistance to them; specifically cucumber plants are
 CC protected against Frankliniella occidentals but the method can be used
 CC for other, esp. parthenocarpic and/or apomictic plants. The plants are
 CC also less susceptible to secondary fungal infection. Elimination of
 CC petals may improve photosynthesis and seed yield may be increased. See
 CC also AAR46556-7. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 16-OCT-2003 to standardise OS field)

XX Sequence 210 AA;

Query Match 62.1%; Score 684.5; DB 2; Length 210;
 Best Local Similarity 62.3%; Pred. No. 2.5e-51;
 Matches 134; Conservative 43; Mismatches 33; Indels 5; Gaps 2;
 QY 1 MGRGKVEIKRIENSSNQVTSYKRRNGIHKAKEITVLCDAKVSIIYSSGGWVEYCSF 60
 DB 1 MGRGKVEIKRIENSSNQVTSYKRRNGIHKAKEITVLCDAKVSIIYSSGGWVEYCSF 60
 QY 61 STTILTEILDKYHGSQGGKLLWDAKHENLSNEVDVKKNDNSQVLEHLKGEDITSLNHVE 120
 DB 59 STSLVDILQYHKLTRRLLDKAKHENLDNEINKYKNDNNQIELRLKGEDITSLNHRE 118
 QY 121 LMALEALENGLTSIRDKQSKFVDMRDNGKALEDENKRLTYELOKQOEMKIKENVRNME 180
 DB 119 LMILEDALNGLTSIRDKQSKFVDMRDNGKALEDENKRLTYELOKQOEMKIKENVRNME 178
 QY 181 NGYHORLGNVNNQOQIPFAFRVQPIQPNLQERI 215
 DB 179 EVFQORENHQYQH--MPPAFRVQPMQPNLQERL 210

RESULT 3

AAG21899

ID AAG21899 standard; protein; 208 AA.

AC AAG21899;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 24625.

XX Protein identification; signal transduction pathway; metabolic pathway;
 XX hybridisation assay; genetic mapping; gene expression control; promoter;
 XX termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

XX 23-MAR-1999; 99US-0125788P.

XX 25-MAR-1999; 99US-0126264P.

XX 29-MAR-1999; 99US-0126785P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 08-APR-1999; 99US-0128714P.

XX 16-APR-1999; 99US-0129845P.

XX 19-APR-1999; 99US-0130077P.

XX 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138840P.
PR 10-JUN-1999; 99US-0138847P.
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PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
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PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139859P.
PR 23-JUN-1999; 99US-0140333P.
PR 23-JUN-1999; 99US-0140334P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142350P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143646P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145244P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
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PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148555P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
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PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 31-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155658P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.

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PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 59.9%; Score 660.5; DB 3; Length 208;
Best Local Similarity 60.5%; Pred. No. 3e-49;
Matches 130; Conservative 33; Mismatches 39; Indels 13; Gaps 2;

QY 1 MGRGKVEIKRIENSNROVTSKRRNGIILKKAKEITVLCDAKVSLLIYSSGGMWVCSP 60
DB 1 MGRGKVEIKRIENSNROVTSKRRNGIILKKAKEITVLCDAKVSLLIYSSGGMWVCSP 60
QY 61 STLTTEILDYKHGSGKKLWDKXENLSNEVDVRVKDNDMSQVLEHLKXGEDITSLNHYE 120
DB 61 SMDLGAMLDQYKLSGKKLWDKXENLSNEVDVRVKDNDMSQVLEHLKXGEDITSLNHYE 120
QY 121 LMALEALENGLSIRDQSKFVDMRDNGKALEDENKELTVELQKQEMKIKENVRNNE 180
DB 121 LMAVEAIEHGLDKVRDHQMEIILSKRNEKMAEEQRLTFLO-QQEMAIASARGMM 179
QY 181 NGYHQRLGNYNNOQQIIPFAFRVQPIQPNLQEI 215
DB 180 MRHDGQ-----FGYRVQPIQPNLQEI 202

RESULT 4
ABG60941
ID ABG60941 standard; protein; 209 AA.
AC ABG60941;
XX
DT 27-AUG-2002 (first entry)
XX
DE Novel floral meristem identity protein LpMADS1.
XX
KW Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
KW HB-like protein; plant growth; plant architecture;
KW inflorescence development; flower development; embryo development;
KW seed development; flower organ identity; phase change; male sterility;
KW hybrid seed production; herbage quality; early maturing crop;
KW biomass increase; branching increase; blocking flowering;
KW allergenic pollen; floral meristem identity protein.
XX
OS Lolium perenne.
XX
XX WO200233091-A1.
XX
XX 25-APR-2002.
XX
XX 17-OCT-2001; 2001WO-AU001311.
XX
XX 19-OCT-2000; 2000AU-00000873.
XX

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PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
XX
PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX
DR WPI; 2002-454601/48.
DR N-PSDB; ABR82124.
XX
PT New substantially purified or isolated polypeptide e.g., MADS-box,
PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
PT fescue species, useful for controlling plant life cycles and/or growth
PT phases.
XX
PS Claim 16; Fig 55; 290pp; English.
XX
CC The invention describes a substantially purified or isolated polypeptide
CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
CC and HB-like proteins, or their functionally active fragments or variants.
CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
CC vector (IV) comprising (II), is useful for modifying plant life cycles
CC and/or growth phases, flowering processes, flowering and/or plant
CC architecture and/or flower and/or inflorescence development in a plant,
CC which involves introducing (II), (III) or (IV) into the plant. The
CC individual or simultaneous enhancement or downregulation of MADS-box gene
CC activities may alter flower, embryo and seed development, e.g., enhance
CC or inhibit embryo differentiation and growth or alter flower organ
CC identity through conversion of one floral organ in another. Manipulation
CC of CEN or HB activity in plants alters the control of phase change,
CC flowering time and the number of leaves made before flowering.
CC Manipulation of AP2 activity in plants alters flower organ identity
CC through conversion of one floral organ in another, leads to a change in
CC the number of floral organs and flowering architecture. Manipulation of
CC flowering plant architecture has a wide range of applications such as:
CC inducing male sterility for hybrid seed production; changing flower
CC architecture for enhancing value of ornamentals; delaying flowering in
CC forage grasses thus stopping the formation of less digestible stems and
CC increasing herbage quality; altering flowering time allowing early
CC maturing crops; delaying vegetative phase to increase biomass production;
CC increasing branching to enhanced business in fruit trees; altering plant
CC size e.g. shorter plant stature; and in blocking flowering and reducing
CC release for allergenic pollen. This is the amino acid sequence of a novel
CC floral meristem identity protein involved in floral development and a
CC potential target for manipulating plant life cycles
XX
SQ Sequence 209 AA;

Query Match 58.9%; Score 650; DB 5; Length 209;
Best Local Similarity 57.3%; Pred. No. 2.5e-48;
Matches 122; Conservative 42; Mismatches 43; Indels 6; Gaps 2;

QY 1 MGRGKVEIKRIENSNROVTSKRRNGIILKKAKEITVLCDAKVSLLIYSSGGMWVCSP 60
DB 1 MGRGKVEIKRIENSNROVTSKRRNGIILKKAKEITVLCDAKVSLLIYSSGGMWVCSP 60
QY 61 STLTTEILDYKHGSGKKLWDKXENLSNEVDVRVKDNDMSQVLEHLKXGEDITSLNHYE 120
DB 61 KTSLSRILEKYQTSNGKILWDEKXLSAEIDRIKKENDNMQIELRHLKXGEDITSLNHYE 120
QY 121 LMALEALENGLSIRDQSKFVDMRDNGKALEDENKELTVELQKQEMKIKENVRNNE 180
DB 121 LIMIEEALNGLTGLHEKQMEHYDRUNKTGKMLEDENKULAFKLH-QQDIALNGNRELE 179
QY 181 NGYHQRLGNYNNOQQIIPFAFRVQPIQPNLQEI 213
DB 180 LGYHPDR-----DFAAQMPITFRVQSPHENLQEI 207

RESULT 5
ABG60932
ID ABG60932 standard; protein; 260 AA.
XX

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AC ABG60932;
 XX 27-AUG-2002 (first entry)
 DT
 DE Novel floral meristem identity protein LpMADS1.
 XX Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein.
 XX
 OS Lolium perenne.
 XX WO200233091-A1.
 PN
 XX 25-APR-2002.
 PD
 XX 17-OCT-2001; 2001WO-AU001311.
 FF
 XX 19-OCT-2000; 2000AU-00000873.
 XX
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 PA
 PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX WPI; 2002-454601/48.
 DR N-PSDB; ABK82086.
 DR
 XX New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 XX
 PS Claim 16; Fig 28; 290pp; English.
 XX
 CC The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (i), a construct (iii) comprising (ii), or a
 CC vector (iv) comprising (ii), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (ii), (iii) or (iv) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced biomass in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This is the amino acid sequence of a novel
 CC floral meristem identity protein involved in floral development and a
 CC potential target for manipulating plant life cycles
 XX
 SQ Sequence 260 AA;

Query Match 58.9%; Score 650; DS 5; Length 260;
 Best Local Similarity 57.3%; Pred. No. 3.4e-48;
 Matches: 122; Conservative 42; Mismatches 43; Indels 6; Gaps 2;
 QY 1 MGROKVEIKRIENSNQVYTSKRNGIHKAKKAITVCDKYSLLIYSSSGKWEYCSF 60
 DB 28 MGRGKIEIKRIENSNQVYTSKRNGIHKAKKAITVCDKYSLLIYSSSGKWEYCSF 87
 QY 61 STLTLEILDKYHGGSGKKLMDAKHENLSNEVDVRVKDNDSDMQVELRHLKGEDITSLNHVE 120
 DB 88 KTSLSRLEKVKQVNSGKILMDKHSLSAIDRAIKKENDNDNQIELRHLKGEDLSLPKE 147
 QY 121 LMALEALENGLTIRDKQSKFVDMEDNDNGKALEDENKRLTYELQKQEMKIKENVTNME 180
 DB 148 LIMTEALDNGLTGLHEKQMEHYDLRMKTGKMLDENKLLAFKLH-QDDIALNGNMLE 206
 QY 181 NGYHQRLQNGVNNNQIIPFAFRVQPIQPNLQE 213
 DB 207 LGYHPDR-----DFAAQNPITFRVQPSHPNLQE 234
 RESULT 6
 ABG60942
 ID ABG60942 standard; protein; 209 AA.
 XX
 AC ABG60942;
 XX 27-AUG-2002 (first entry)
 DT
 DE Novel floral meristem identity protein LpMADS1b.
 XX
 KW Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KW HB-like protein; plant growth; plant architecture;
 KW inflorescence development; flower development; embryo development;
 KW seed development; flower organ identity; phase change; male sterility;
 KW hybrid seed production; herbage quality; early maturing crop;
 KW biomass increase; branching increase; blocking flowering;
 KW allergenic pollen; floral meristem identity protein.
 XX
 OS Lolium perenne.
 XX WO200233091-A1.
 PN
 XX 25-APR-2002.
 PD
 XX 17-OCT-2001; 2001WO-AU001311.
 FF
 XX 19-OCT-2000; 2000AU-00000873.
 XX
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRE-) AGRESEARCH LTD.
 PA
 PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX WPI; 2002-454601/48.
 DR N-PSDB; ABK82125.
 DR
 XX New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 XX
 PS Claim 16; Fig 60; 290pp; English.
 XX
 CC The invention describes a substantially purified or isolated polypeptide
 CC (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
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 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (i), a construct (iii) comprising (ii), or a
 CC vector (iv) comprising (ii), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (ii), (iii) or (iv) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced biomass in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This is the amino acid sequence of a novel
 CC floral meristem identity protein involved in floral development and a
 CC potential target for manipulating plant life cycles
 XX
 SQ Sequence 260 AA;

architecture and/or flower and/or inflorescence development in a plant, which involves introducing (II), (III) or (IV) into the plant. The individual or simultaneous enhancement or downregulation of MADS-box gene activities may alter flower, embryo and seed development, e.g., enhance or inhibit embryo differentiation and growth or alter flower organ identity through conversion of one floral organ in another. Manipulation of CEN or HB activity in plants alters the control of phase change, flowering time and the number of leaves made before flowering. Manipulation of AP2 activity in plants alters flower organ identity through conversion of one floral organ in another, leads to a change in the number of floral organs and flowering architecture. Manipulation of flowering plant architecture has a wide range of applications such as: inducing male sterility for hybrid seed production; changing flower architecture for enhancing value of ornamentals; delaying flowering in forage grasses thus stopping the formation of less digestible stems and increasing herbage quality; altering flowering time allowing early maturing crops; delaying vegetative phase to increase biomass production; increasing branching to enhanced business in fruit trees; altering plant size e.g. shorter plant stature; and in blocking flowering and reducing release for allergenic pollen. This is the amino acid sequence of a novel floral meristem identity protein involved in floral development and a potential target for manipulating plant life cycles

XX SQ Sequence 209 AA;

Query Match 58.5%; Score 645; DB 5; Length 209;
Best Local Similarity 57.3%; Pred. No. 6.8e-48;
Matches 122; Conservative 41; Mismatches 44; Indels 6; Gaps 2;
Qy 1 MGRGKVEIKRIENSNRQVTSKRRNGIITKAKEITVLCDAKVSLIYSSGKRWVEYCSF 60
Db 1 MGRGKVEIKRIENSNRQVTSKRRNGIITKAKEITVLCDAKVSLIYSSGKRWVEYCSF 60
Qy 61 STLTITLTDYKHGSGKGLWDKHNLSNEVDKNDNDSDMOVELHKLKGEDITSLNHYE 120
Db 61 KTSLSRILEKYQNTSKILWDEKHSLSAEIDRIKENNDNMQIELHLKGEDINSLOPKX 120
Qy 121 LMALEBALNGLTSIRDKSKFVDMRDNGKALEDENKELTYELOQOQEMKIKENVRNME 180
Db 121 LIMIEBALDNLGLTGLHEKQMEHYDRLMTKGMLENDENKLLASKLH-QQDIALNGNRELE 179
Qy 181 NGVHQRLGNYNNOQOIPPAFRVQIPQNLQE 213
Db 180 LGVHPDR-----DFAAQMPITFRVQPSHENLQE 207

RESULT 7
ABG60945

ID ABG60945 standard; protein; 209 AA.

XX AC ABG60945;

XX DT 27-AUG-2002 (first entry)

XX DE Novel floral meristem identity protein LpMADS2-3.

XX KW Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
XX KW CEN-like protein; APEAL2; AP2; AP2-like protein; HB; Homeo-box protein;
XX KW HB-like protein; plant growth; plant architecture;
XX KW inflorescence development; flower development; embryo development;
XX KW seed development; flower organ identity; phase change; male sterility;
XX KW hybrid seed production; herbage quality; early maturing crop;
XX KW biomass increase; branching increase; blocking flowering;
XX KW allergenic pollen; floral meristem identity protein.

OS Lolium perenne.

XX WO200233091-A1.

XX PD 25-APR-2002.

XX PF 17-OCT-2001; 2001WO-AU001311.

PR 19-OCT-2000; 2000AU-00000873.
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRISearch LTD.
XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
PI WPI; 2002-454601/48.
XX N-PSDB; ABK82128.
DR New substantially purified or isolated polypeptide e.g., MADS-box,
XX CENTRORADIALIS, APEAL2, Homeo-box proteins, isolated from ryegrass or
PT fescue species, useful for controlling plant life cycles and/or growth
PT phases.
XX Claim 16; Fig 73; 290pp; English.

The invention describes a substantially purified or isolated polypeptide (I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like proteins, APEAL2 (AP2) and AP2-like proteins, Homeo-box proteins (HB) and HB-like proteins, or their functionally active fragments or variants. Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a vector (IV) comprising (II), is useful for modifying plant life cycles and/or growth phases, flowering processes, flowering and/or plant architecture and/or flower and/or inflorescence development in a plant, which involves introducing (II), (III) or (IV) into the plant. The individual or simultaneous enhancement or downregulation of MADS-box gene activities may alter flower, embryo and seed development, e.g., enhance or inhibit embryo differentiation and growth or alter flower organ identity through conversion of one floral organ in another. Manipulation of CEN or HB activity in plants alters the control of phase change, flowering time and the number of leaves made before flowering. Manipulation of AP2 activity in plants alters flower organ identity through conversion of one floral organ in another, leads to a change in the number of floral organs and flowering architecture. Manipulation of flowering plant architecture has a wide range of applications such as: inducing male sterility for hybrid seed production; changing flower architecture for enhancing value of ornamentals; delaying flowering in forage grasses thus stopping the formation of less digestible stems and increasing herbage quality; altering flowering time allowing early maturing crops; delaying vegetative phase to increase biomass production; increasing branching to enhanced business in fruit trees; altering plant size e.g. shorter plant stature; and in blocking flowering and reducing release for allergenic pollen. This is the amino acid sequence of a novel floral meristem identity protein involved in floral development and a potential target for manipulating plant life cycles

XX SQ Sequence 209 AA;

Query Match 58.0%; Score 640; DB 5; Length 209;
Best Local Similarity 56.8%; Pred. No. 1.8e-47;
Matches 121; Conservative 41; Mismatches 45; Indels 6; Gaps 2;
Qy 1 MGRGKVEIKRIENSNRQVTSKRRNGIITKAKEITVLCDAKVSLIYSSGKRWVEYCSF 60
Db 1 MGRGKVEIKRIENSNRQVTSKRRNGIITKAKEITVLCDAKVSLIYSSGKRWVEYCSF 60
Qy 61 STLTITLTDYKHGSGKGLWDKHNLSNEVDKNDNDSDMOVELHKLKGEDITSLNHYE 120
Db 61 KTSLSRILEKYQNTSKILWDEKHSLSAEIDRIKENNDNMQIELHLKGEDINSLOPKX 120
Qy 121 LMALEBALNGLTSIRDKSKFVDMRDNGKALEDENKELTYELOQOQEMKIKENVRNME 180
Db 121 LIMIEBALDNLGLTGLHEKQMEHYDRLMTKGMLENDENKLLASKLH-QQDIALNGNRELE 179
Qy 181 NGVHQRLGNYNNOQOIPPAFRVQIPQNLQE 213
Db 180 LGVHPDR-----DFAAQMPITFRVQPSHENLQE 207

RESULT 8
AAG40904


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Db      121 LIMTEALDGLNLNKLMEHWRVNTKMMEDENKULAFKLH-QQDIALSGSMRELE 179
Qy      181 NGYH-QRELGNVNNQOQIFFAFRVQPIQPNLOE 213
Db      180 LGVHPDRDLA-----AQMPTTRVQPSHPNLOE 207

RESULT 10
AAG21900
ID   AAG21900 standard; protein; 155 AA.
XX
AC   AAG21900;
XX
DT   17-OCT-2000 (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 24626.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EPI033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-00301439.
XX
PR   25-FEB-1999; 99US-0121825P.
PR   05-MAR-1999; 99US-0123180P.
PR   09-MAR-1999; 99US-0123548P.
PR   23-MAR-1999; 99US-0125788P.
PR   25-MAR-1999; 99US-0126264P.
PR   29-MAR-1999; 99US-0126785P.
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PR   28-APR-1999; 99US-0130891P.
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PR   04-MAY-1999; 99US-0132484P.
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PR   06-MAY-1999; 99US-0132486P.
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PR   01-JUL-1999; 99US-0141842P.
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PR   05-AUG-1999; 99US-0147192P.
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PR   06-AUG-1999; 99US-0147303P.
PR   06-AUG-1999; 99US-0147416P.
PR   09-AUG-1999; 99US-0147493P.
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PR   10-AUG-1999; 99US-0148171P.
PR   11-AUG-1999; 99US-0148319P.
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PR 12-AUG-1999; 99US-0148341P.
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 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
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 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.
 PR 29-OCT-1999; 99US-0162143P.

Query Match 39.5%; Score 435.5; DB 3; Length 155;
 Best Local Similarity 54.3%; Pred. No. 7.2e-30;
 Matches 8; Conservative 23; Mismatches 38; Indels 13; Gaps 2;

QY 54 MRYCSPSTLTILDKYHQSCKLWDAKHENLSNEVDRVKDNDMSQVLRHLKGEDI 113
 Db 1 MIDYCCPMDLGMLDQYQKLSGKCLWDAKHENLSNEIDRIKENDSLQLELRHLKGEDI 60

QY 114 TSLNHVELMALPEALENGLTSTRDKQSKFVDMRDNKGALDENKRLTYELQKQOEMKIK 173
 Db 61 QSLNLKMLMAVEHAIEHGLDKVRDHQMEILISKRENEQMAEEQRQLTFQLQ-QQMAIA 119

QY 174 ENVRNMENGYHORGLGNYNNNQQQIPFAFRVQPIQPNLQERI 215
 Db 120 SNARGMMRRDHGQ-----FGYRVQPIQPNLQEKI 149

RESULT 11
 AAE25763
 ID AAE25763 standard; protein; 224 AA.
 XX
 AC AAE25763;
 XX
 DT 04-NOV-2002 (first entry)
 XX
 DE Rice MADS box-like protein.
 XX
 KW Floral developmental protein; flowering locus T; APETALA3; transgenic;
 KW FT; AP3; transgenic plant; fertility; flower development; gene mapping;
 KW sterility; plant growth; inflorescence architecture; plant morphology;
 KW tissue culture; cell division; rice; MADS box-like protein.
 XX
 OS Oryza sativa.
 XX
 PN WO200244390-A2.
 XX
 PD 06-JUN-2002.
 XX
 PF 21-NOV-2001; 2001WO-US043750.
 XX
 PR 28-NOV-2000; 2000US-0253445P.
 XX
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;
 XX
 DR WPI; 2002-547703/58.
 XX
 PT New floral developmental polypeptide having flowering locus T or Ap3
 PT homolog activity, useful for immunological screening of cDNA expression
 PT libraries.
 XX
 PS Example 4; Page 82-83; 88pp; English.
 XX
 CC The present invention relates to novel floral developmental proteins,
 CC more specifically flowering locus T (FT) or APETALA3 (AP3) homologous
 CC proteins and polynucleotides encoding such proteins. Floral developmental
 CC polynucleotides are useful for transforming cells or for producing plants
 CC by transforming the plant cells with the polynucleotides and regenerating
 CC the plants from the transformed plant cells. Sequences of the invention
 CC are useful for immunological screening of cDNA expression libraries. They
 CC are also useful for creating transgenic plants. Polynucleotides of the
 CC invention are used as probes for genetically and physically mapping the
 CC genes that they are a part of and as markers for traits linked to those
 CC genes. AP3 homologues may be useful for engineering plant sterility or
 CC fertility, flower development and morphology. FT or TFL1 homologues are
 CC useful for engineering flowering time, plant growth rate, inflorescence
 CC architecture, tissue culture morphology and rate of cell division to
 CC enhance transformation. The present sequence is rice MADS box-like
 CC protein. This sequence is used in the exemplification of the invention
 XX
 SQ Sequence 224 AA;

Qy 61 STILTEILDKYHSGSKKLINDAKHENLSNEVDKVKDNDMSQVELRHLKGEDTISLHV 120
Db 61 STDIKGFIDRYQQAIGTSLIEQYENMQRTLSHLKDINRLRTEIQRMGEDLDGLEFDE 120
Qy 121 LMALEEALENGLTSIRDKQSKFVDMMDRDNGKALEDENKRLTYELQK--QOEMKIKEN--- 175
Db 121 LRGLEQNVDAALKREVRHKYHVTQTETK----KKVHSYEAYETLQOELGLREPAF 176
Qy 176 --VRNMENGHQRLGNYYNNQQOIPAPRVQPIQPNL 211
Db 177 GFVDNTGGWD---GGAGAGAAADMFAPRVFSQPNL 210

RESULT 12
AAG21901
ID AAG21901 standard; protein; 147 AA.
XX AC AAG21901;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 24627.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; Genetic mapping; gene expression control; promoter;
XX termination sequence.
XX OS Arabidopsis thaliana.
XX EN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 29-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127452P.
PR 06-APR-1999; 99US-0128253P.
PR 08-APR-1999; 99US-0128714P.
PR 19-APR-1999; 99US-0129845P.
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PR 21-APR-1999; 99US-0130449P.
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PR 04-MAY-1999; 99US-0132484P.
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PR 10-JUN-1999; 99US-0138540P.
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PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
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PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
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PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 22-JUL-1999; 99US-0145193P.
PR 22-JUL-1999; 99US-0145194P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.

Matches	78; Conservative	52; Mismatches	76; Indels	8; Gaps	3;
Qy	1 MGRGKVIKRIENSSNQVTSYKERNGLIIKAKKAITVLCDAKVSLLIYSSSGKMWYECSP	60			
Db	1 MARGKIQIKRIENNTNRQVTSYKERNGLFKKANELTVLCDAKVSIIIFSSSTGKLHQYISP	60			
Qy	61 STTLTEILDYHGSGKGLWDAKHENLSNEVDYVKKNDMSQVLRHLKGEDITSLNHYE	120			
Db	61 STSTKQFFDQYQWTLGVDLNNSHYENQENLKKLKEVNRNLKEIRQRMGDCNLNMGED	120			
Qy	121 LMALEEALENGLTISIRDKQSKF----	VDMMRDNGKALEDENKRLTYELQKQOEMKIKENV	176		
Db	121 LKLEEEEMDKAAKVVREKRYKVIITNQIDTQKKFNNEKEVHNRLHLDLDAKAE--DPRF	177			
Qy	177 RNMENGYHQROLGNYNQOQIPAFRVQPIQPN	210			
Db	178 ALIDNGGEYSVIGFSNLGPRM-FALSIQFSHP	210			

Search completed: September 27, 2004, 09:25:11
 Job time : 90.6152 secs

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OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 20:24:57 ; Search time 455.966 Seconds
(without alignments)
9149.204 Million cell updates/sec

Title: US-10-069-527-3

Perfect score: 982

Sequence: 1 atggcgccggaagattga.....aaaaaaaaaaaaaaaaaaaaa 982

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 1000 summaries

Database : N_Geneseq_29Jan04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002s.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	982	100.0	982	4	AAS00104
2	28	2.9	1447	7	ACA96031
3	27	2.7	121	6	ABK25242
4	27	2.7	121	6	ABK25241
5	27	2.7	121	6	ABK25237
6	27	2.7	121	6	ABK25238
7	27	2.7	390	8	ACH38095
8	27	2.7	448	7	ABK60903
9	27	2.7	458	6	ABL93709
10	27	2.7	712	6	ABQ65619
11	27	2.7	980	4	AD06338
12	27	2.7	1167	2	AAT66687
13	27	2.7	1167	2	AAV69276
14	27	2.7	1167	2	AAV81423
15	27	2.7	1167	8	ADA01011
16	27	2.7	1547	6	ABN84158
17	27	2.7	17424	6	ABL68122
18	26	2.6	121	6	ABK25462
19	26	2.6	121	6	ABK25466
20	26	2.6	121	6	ABK25465
21	26	2.6	121	6	ABK25461
22	26	2.6	164	9	ADE58862
23	26	2.6	181	7	ACC60003

24	26	2.6	267	7	ACA05130	ACA05130 Rice leaf
25	26	2.6	461	6	ABL93649	ABL93649 Arabidops
26	26	2.6	487	8	ACH34795	ACH34795 Human end
27	26	2.6	552	6	ABQ57750	ABQ57750 Human col
28	26	2.6	868	4	AAS00103	AAS00103 Granny Sm
29	26	2.6	1142	6	ABN98309	ABN98309 Arabidops
30	26	2.6	1154	2	AAT39048	AAT39048 cDNA enco
31	26	2.6	1306	6	AAD42765	AAD42765 Wheat GGP
32	26	2.6	1306	6	ACA05162	ACA05162 Wheat ger
33	26	2.6	1770	5	AAF24163	AAF24163 Human sec
34	26	2.6	1819	5	AAF30436	AAF30436 Rice apop
35	26	2.6	1978	2	AAQ37189	AAQ37189 Petunia E
36	26	2.6	2645	3	AAF16125	AAF16125 Human pro
37	26	2.6	2663	4	AAD08310	AAD08310 Human sec
38	26	2.6	2844	7	ABT31903	ABT31903 Human bpc
39	26	2.6	80578	4	AAH44800	AAH44800 Human GPC
40	25	2.5	44	6	AAS17877	AAS17877 FC-3 comm
41	25	2.5	45	8	ABZ76605	ABZ76605 Human CNI
42	25	2.5	51	4	AAI29700	AAI29700 Human SNP
43	25	2.5	207	6	ABU86102	ABU86102 Human ova
44	25	2.5	269	7	ABX61308	ABX61308 Arabidops
45	25	2.5	394	5	ABV49244	ABV49244 Human pro
46	25	2.5	396	4	AAF94886	AAF94886 Human ova
47	25	2.5	396	6	ABU48836	ABU48836 Ovarian c
48	25	2.5	423	3	ABT03153	ABT03153 Human ova
49	25	2.5	458	8	ACH21953	ACH21953 Human hea
50	25	2.5	502	5	ABV56360	ABV56360 Human pro
51	25	2.5	524	2	AAQ12088	AAQ12088 C-termina
52	25	2.5	650	3	ACA59569	ACA59569 Human sec
53	25	2.5	878	4	AAK64702	AAK64702 Human imm
54	25	2.5	1145	6	ABK35955	ABK35955 cDNA sequ
55	25	2.5	1146	2	AAZ07000	AAZ07000 Xenopus F
56	25	2.5	1190	2	AAZ20289	AAZ20289 Aspen hom
57	25	2.5	1347	4	AAZ86035	AAZ86035 CABP-1 co
58	25	2.5	1392	6	AAZ39218	AAZ39218 Rice tyro
59	25	2.5	1402	2	AAZ78204	AAZ78204 Soybean N
60	25	2.5	1402	4	AAZ57653	AAZ57653 Soybean i
61	25	2.5	1487	3	AAZ41288	AAZ41288 Human nor
62	25	2.5	1760	3	AAZ43782	AAZ43782 Human fec
63	25	2.5	1796	8	ABZ76577	ABZ76577 Human CNI
64	25	2.5	1940	2	AAZ38690	AAZ38690 Mouse CRT
65	25	2.5	1974	7	ADA56170	ADA56170 Gene enco
66	25	2.5	1974	7	ADA39981	ADA39981 Human sec
67	25	2.5	1974	7	ACC50542	ACC50542 Human sec
68	25	2.5	1974	9	ADC73606	ADC73606 Human sec
69	25	2.5	1981	3	AAZ34558	AAZ34558 cDNA enco
70	25	2.5	2133	9	ADD44818	ADD44818 Rat gene
71	25	2.5	2133	9	ADD44822	ADD44822 Rat gene
72	25	2.5	2149	2	AAZ87942	AAZ87942 Human cys
73	25	2.5	2149	2	ACC00727	ACC00727 Zea mays
74	25	2.5	2290	6	ABK35014	ABK35014 Human CDN
75	25	2.5	2359	9	ADB52957	ADB52957 Primary r
76	25	2.5	2396	2	AAV66452	AAV66452 An antidi
77	25	2.5	2396	2	AAZ35295	AAZ35295 Nucleic a
78	25	2.5	2396	2	AAZ35295	AAZ35295 Nucleic a
79	25	2.5	2396	3	AAA07264	AAA07264 Rice prob
80	25	2.5	2396	3	AAA07264	AAA07264 Rice prob
81	25	2.5	3056	6	ABZ57331	ABZ57331 cDNA enco
82	25	2.5	4131	2	AAZ89290	AAZ89290 Dogfish s
83	25	2.5	4134	6	AAZ41631	AAZ41631 SKCar DNA
84	25	2.5	4134	6	ABK14910	ABK14910 DNA enco
85	25	2.5	4134	6	ABL59964	ABL59964 Dogfish s
86	25	2.5	34658	4	AAK69489	AAK69489 Human imm
87	25	2.5	40	2	AAQ22625	AAQ22625 Sense oli
88	24	2.4	47	3	AAA61350	AAA61350 Model lin
89	24	2.4	47	4	AAV60446	AAV60446 DNA oligo
90	24	2.4	97	2	AAV68582	AAV68582 Nucleotid
91	24	2.4	101	2	AAT07155	AAT07155 pV3TA-LTR
92	24	2.4	121	6	ABK25234	ABK25234 Male-ster
93	24	2.4	121	6	ABK25234	ABK25234 Male-ster
94	24	2.4	121	6	ABK25265	ABK25265 Male-ster
95	24	2.4	121	6	ABK25269	ABK25269 Male-ster
96	24	2.4	121	6	ABK25270	ABK25270 Male-ster

97	24	2.4	121	6	ABK25273	Abk25273 Male-ster	170	24	2.4	1093	7	ABZ67043	Abz67043 Human sec
98	24	2.4	121	6	ABK25266	Abk25266 Male-ster	171	24	2.4	1093	7	ADA43901	Ada43901 Human sec
99	24	2.4	121	6	ABK25274	Abk25274 Male-ster	172	24	2.4	1133	3	Aaz90586	Aaz90586 Maize pro
100	24	2.4	121	6	ABK25233	Abk25233 Male-ster	173	24	2.4	1201	2	AAX61465	AAX61465 DNA encod
101	24	2.4	121	6	ABK25262	Abk25262 Male-ster	174	24	2.4	1344	4	Aah72881	Aah72881 Human cer
102	24	2.4	121	6	ABK25261	Abk25261 Male-ster	175	24	2.4	1344	4	AaQ44450	AaQ44450 Cysteine
103	24	2.4	166	2	AAQ67613	AaQ67613 tRNA modi	176	24	2.4	1305	7	ADA09070	Ada09070 DNA encod
104	24	2.4	166	2	AAQ67614	AaQ67614 tRNA modi	177	24	2.4	1323	3	AAa61764	AAa61764 cDNA encod
105	24	2.4	169	4	AA524514	AA524514 Human ova	178	24	2.4	1430	3	AAX90911	AAX90911 Human cDN
106	24	2.4	170	5	AAH83122	AAH83122 Human ova	179	24	2.4	1439	2	AAQ92086	AAQ92086 Human rec
107	24	2.4	185	5	ABV34436	ABV34436 Human pro	180	24	2.4	1439	2	AzO97669	AzO97669 Human CD1
108	24	2.4	185	5	ABV43294	ABV43294 Human pro	181	24	2.4	1486	3	AAc98137	AAc98137 Human col
109	24	2.4	192	7	ABZ78104	ABZ78104 Human sup	182	24	2.4	1507	6	ABs54111	ABs54111 Tobacco c
110	24	2.4	201	6	ABL85925	ABL85925 Human ova	183	24	2.4	1564	7	ABX78356	ABX78356 Soybean s
111	24	2.4	235	7	ABX68003	ABX68003 Arabidops	184	24	2.4	1565	8	ADD17505	ADD17505 Wheat pos
112	24	2.4	250	7	ABX98053	ABX98053 Rice endo	185	24	2.4	1588	9	ADD14723	ADD14723 Human src
113	24	2.4	293	2	AAAT07148	AAAT07148 Ribozyme-	186	24	2.4	1607	2	AAx60316	AAx60316 DNA encod
114	24	2.4	293	2	AAAT07152	AAAT07152 Ribozyme-	187	24	2.4	1624	2	AAAT39750	AAAT39750 Human muc
115	24	2.4	293	2	AAAT07151	AAAT07151 Ribozyme-	188	24	2.4	1624	2	AAx35279	AAx35279 cDNA enco
116	24	2.4	293	2	AAAT07147	AAAT07147 Ribozyme-	189	24	2.4	1646	6	ABQ88122	ABQ88122 Human est
117	24	2.4	300	2	AAQ67610	AAQ67610 PV3TA-tat	190	24	2.4	1702	4	AAc85066	AAc85066 Atheroscl
118	24	2.4	300	2	AAQ67609	AAQ67609 PV3TA-LTR	191	24	2.4	1734	4	AAAT39792	AAAT39792 Human SH3
119	24	2.4	326	4	AAAL28279	AAAL28279 Human bre	192	24	2.4	1749	4	AAI60696	AAI60696 Human pol
120	24	2.4	328	4	AAAL08534	AAAL08534 Human bre	193	24	2.4	1755	2	AAAT91321	AAAT91321 Arabidops
121	24	2.4	345	2	AAQ67612	AAQ67612 PV3TA-tat	194	24	2.4	1760	3	AAc59930	AAc59930 Human sec
122	24	2.4	346	2	AAQ94618	AAQ94618 PV3TA-tat	195	24	2.4	1795	3	AAf18075	AAf18075 Lung canc
123	24	2.4	348	2	AAQ67611	AAQ67611 PV3TA-tat	196	24	2.4	1795	3	AAf18075	AAf18075 Lung canc
124	24	2.4	354	7	ABZ73127	ABZ73127 Rice leaf	197	24	2.4	1971	2	AAx08428	AAx08428 Acidic le
125	24	2.4	368	4	AAAL19229	AAAL19229 Human bre	198	24	2.4	2069	1	AAAT92452	AAAT92452 cDNA inse
126	24	2.4	374	4	AAAS25015	AAAS25015 Human ova	199	24	2.4	2125	6	AAc59087	AAc59087 Human sec
127	24	2.4	374	5	AAH83660	AAH83660 Human ova	200	24	2.4	2125	6	AAc59087	AAc59087 Human sec
128	24	2.4	381	7	ABZ73087	ABZ73087 Rice leaf	201	24	2.4	2185	3	AAf05130	AAf05130 Cytokine
129	24	2.4	390	8	ACH29210	ACH29210 Human adu	202	24	2.4	2187	3	AAZ922220	AAZ922220 Human thi
130	24	2.4	391	2	AAQ94619	AAQ94619 PV3TA-tat	203	24	2.4	2187	6	AAI72961	AAI72961 Human thi
131	24	2.4	391	4	AAH33291	AAH33291 Human col	204	24	2.4	2203	2	AAZ06247	AAZ06247 Human sec
132	24	2.4	395	7	ABX62795	ABX62795 Arabidops	205	24	2.4	2217	9	ABT42483	ABT42483 Toxicity
133	24	2.4	404	8	ACH18231	ACH18231 Human adu	206	24	2.4	2217	9	ABT42483	ABT42483 Toxicity
134	24	2.4	439	5	ABV48426	ABV48426 Human pro	207	24	2.4	2298	7	ABQ84310	ABQ84310 Human DPP
135	24	2.4	448	2	AAQ94620	AAQ94620 pTAR-PRE-	208	24	2.4	2434	7	ABQ77389	ABQ77389 Human AMP
136	24	2.4	448	3	AAc97748	AAc97748 Bridge-1	209	24	2.4	2480	4	AAAD06509	AAAD06509 Human CON
137	24	2.4	465	6	ABN94845	ABN94845 Gene #134	210	24	2.4	2538	6	AAAD21883	AAAD21883 Human TM4
138	24	2.4	474	7	AAQ03413	AAQ03413 Nucleotid	211	24	2.4	2700	8	AAAL62908	AAAL62908 Soybean c
139	24	2.4	486	7	ABZ73042	ABZ73042 Rice leaf	212	24	2.4	3213	2	AAV55742	AAV55742 Human sec
140	24	2.4	489	7	ACC60406	ACC60406 Rice leaf	213	24	2.4	3213	6	AAQ92068	AAQ92068 Human pol
141	24	2.4	515	5	ACC60292	ACC60292 Rice endo	214	24	2.4	3360	4	ABL26030	ABL26030 Drosophil
142	24	2.4	516	5	ABV13318	ABV13318 Human pro	215	24	2.4	4074	6	ABI19626	ABI19626 Mouse isc
143	24	2.4	521	6	ABK54955	ABK54955 Human col	216	24	2.4	6582	9	ABQ74268	ABQ74268 Human 670
144	24	2.4	526	7	ABK59473	ABK59473 Rice albu	217	24	2.4	6582	9	ABQ74268	ABQ74268 Human tra
145	24	2.4	527	7	ACC55423	ACC55423 Rice endo	218	24	2.4	1388	4	ABL05670	ABL05670 Drosophil
146	24	2.4	535	5	ABV48043	ABV48043 Human pro	219	24	2.4	18011	6	ABL32034	ABL32034 Human imm
147	24	2.4	545	5	ABX98574	ABX98574 Rice leaf	220	24	2.4	50000	3	AAAG6363	AAAG6363 Polymorph
148	24	2.4	578	2	AAQ67607	AAQ67607 PV3TA-LTR	221	24	2.4	90220	4	ABK83576	ABK83576 Human cDN
149	24	2.4	595	3	AAAL6271	AAAL6271 Human col	222	24	2.4	40	4	AAH20341	AAH20341 HRV6 viru
150	24	2.4	604	7	ABX78368	ABX78368 Wheat str	223	23	2.3	51	4	AAAL30739	AAAL30739 Human SNP
151	24	2.4	637	4	AAAL15507	AAAL15507 Human bre	224	23	2.3	51	4	AAAL32426	AAAL32426 Human SNP
152	24	2.4	662	6	ABQ57172	ABQ57172 Human col	225	23	2.3	51	4	AAAL27842	AAAL27842 Human SNP
153	24	2.4	685	6	AAAL37825	AAAL37825 Rice KCP-	226	23	2.3	114	4	AAK55505	AAK55505 Human imm
154	24	2.4	690	7	ACA04882	ACA04882 Rice cDNA	227	23	2.3	119	6	ABV96775	ABV96775 Human pan
155	24	2.4	692	2	AAV65762	AAV65762 Pathogen	228	23	2.3	121	6	ABK25162	ABK25162 Male-ster
156	24	2.4	695	8	ADA21181	ADA21181 Human sec	229	23	2.3	121	6	ABK25161	ABK25161 Male-ster
157	24	2.4	756	4	AAAL24351	AAAL24351 Human bre	230	23	2.3	130	4	AA556565	AA556565 Human cDN
158	24	2.4	765	3	AAc59300	AAc59300 Human sec	231	23	2.3	130	7	ABX50278	ABX50278 Bovine ES
159	24	2.4	784	9	ADe62179	ADe62179 Human gen	232	23	2.3	158	4	AAAL34673	AAAL34673 Human mus
160	24	2.4	802	4	AAI94794	AAI94794 Human neu	233	23	2.3	158	7	ABX57661	ABX57661 cDNA enco
161	24	2.4	817	2	AAZ16657	AAZ16657 Human gen	234	23	2.3	159	4	AAK56708	AAK56708 Human imm
162	24	2.4	890	3	AAZ50159	AAZ50159 Corn Aden	235	23	2.3	161	6	ABL86196	ABL86196 Human ova
163	24	2.4	898	4	AAAS33229	AAAS33229 DNA encod	236	23	2.3	202	6	ABL85969	ABL85969 Human ova
164	24	2.4	923	2	AAV04582	AAV04582 Flea seri	237	23	2.3	203	7	ABX49827	ABX49827 Bovine ES
165	24	2.4	1004	6	AAH78831	AAH78831 Human rib	238	23	2.3	270	7	ABZ72981	ABZ72981 Rice leaf
166	24	2.4	1004	6	AA515495	AA515495 DNA encod	239	23	2.3	275	2	AAQ60278	AAQ60278 Human bra
167	24	2.4	1004	8	ACD27686	ACD27686 Human cDN	240	23	2.3	276	6	ABL86284	ABL86284 Human ova
168	24	2.4	1079	9	ADD48673	ADD48673 Human gen	241	23	2.3	276	7	ACC60351	ACC60351 Rice leaf
169	24	2.4	1093	3	AAc59720	AAc59720 Human sec	242	23	2.3	284	5	ABV38207	ABV38207 Human pro

243	23	2.3	288	6	ABQ57354	Human col	316	23	2.3	519	6	ABQ24717	Oligonucle
244	23	2.3	289	6	ABL87876	Human ova	317	23	2.3	519	6	ABK54880	Human col
245	23	2.3	290	6	ABK44641	CDNA enco	318	23	2.3	521	5	AAS09044	Human MEK
246	23	2.3	291	6	ABK46022	CDNA enco	319	23	2.3	531	5	ABV61705	Human pro
247	23	2.3	292	6	ABV97630	Human pan	320	23	2.3	531	5	ABV49683	Human pro
248	23	2.3	293	6	ABV57650	Human ova	321	23	2.3	531	6	ABL38044	Human col
249	23	2.3	294	8	ACH34179	Human end	322	23	2.3	533	6	ABQ58979	Human col
250	23	2.3	295	8	ACH34179	Human end	323	23	2.3	534	7	ACA10307	Rice leaf
251	23	2.3	296	5	ACH97730	Bridge-1	324	23	2.3	535	7	ABZ73036	Rice leaf
252	23	2.3	297	5	ABV49040	Human pro	325	23	2.3	537	6	ABV96144	Human pan
253	23	2.3	298	5	ACH97752	Bridge-1	326	23	2.3	544	7	ACC60103	Rice leaf
254	23	2.3	299	3	ACH97733	Bridge-1	327	23	2.3	545	3	AZ80422	Human col
255	23	2.3	300	5	ABV58492	Human pro	328	23	2.3	576	7	ABX81460	Arabidops
256	23	2.3	301	6	ABL65547	Lung canc	329	23	2.3	576	7	ABX56870	Arabidops
257	23	2.3	302	7	ABL66019	Lung canc	330	23	2.3	589	4	AAH10768	Human CDN
258	23	2.3	303	7	ABX49797	Bovine BS	331	23	2.3	590	4	AAK58428	Human imm
259	23	2.3	304	3	AAA70159	Plasmodiu	332	23	2.3	602	6	ABQ30024	Oligonucle
260	23	2.3	305	6	ABL77085	Human ova	333	23	2.3	602	6	ABQ30025	Oligonucle
261	23	2.3	306	8	ACH32550	Human end	334	23	2.3	602	6	ABN73413	Bovine em
262	23	2.3	307	7	ABX46789	Bovine BS	335	23	2.3	623	6	ABQ52237	Oligonucle
263	23	2.3	308	5	ABV37757	Human pro	336	23	2.3	623	6	ABQ52236	Oligonucle
264	23	2.3	309	5	ABV07659	Human pro	337	23	2.3	627	6	ABQ52242	Oligonucle
265	23	2.3	310	6	AAS61750	Lung smal	338	23	2.3	627	6	ABZ15972	Arabidops
266	23	2.3	311	9	ADDE6939	Human lun	339	23	2.3	630	6	ABZ15972	Arabidops
267	23	2.3	312	9	ADDE6939	Human lun	340	23	2.3	630	6	ABZ15156	Arabidops
268	23	2.3	313	3	ACH33828	Cat flea	341	23	2.3	636	6	ABQ42937	Oligonucle
269	23	2.3	314	7	ABX35859	Bovine BS	342	23	2.3	636	6	ABQ42936	Oligonucle
270	23	2.3	315	7	ACC55387	Rice endo	343	23	2.3	646	6	ABQ66002	Arabidops
271	23	2.3	316	8	ACH35080	Human end	344	23	2.3	658	3	AAC59128	Human sec
272	23	2.3	317	4	AAS60291	Human can	345	23	2.3	668	6	ABQ60251	Human col
273	23	2.3	318	6	ABG58394	Human col	346	23	2.3	678	6	ABQ34133	Human sec
274	23	2.3	319	5	AAF67426	Novel hum	347	23	2.3	681	4	AAF85393	Nucleotid
275	23	2.3	320	7	ABX62416	Arabidops	348	23	2.3	712	3	AAC64050	Trypanoso
276	23	2.3	321	5	ABV49108	Human pro	349	23	2.3	744	3	AAC95537	Human sec
277	23	2.3	322	4	ABX62296	Arabidops	350	23	2.3	764	3	AAC95537	Human sec
278	23	2.3	323	5	AAH88021	Peppermin	351	23	2.3	772	4	AAL24956	Human bre
279	23	2.3	324	5	AAH88021	Peppermin	352	23	2.3	786	6	ABQ33463	Oligonucle
280	23	2.3	325	4	AAL02612	Human rep	353	23	2.3	786	6	ABQ33462	Oligonucle
281	23	2.3	326	5	ABV57920	Human pro	354	23	2.3	822	6	ABQ51819	Oligonucle
282	23	2.3	327	8	ACH25904	Human ova	355	23	2.3	822	6	ABQ44852	Oligonucle
283	23	2.3	328	5	AAH83092	Human ova	356	23	2.3	822	6	ABQ51818	Oligonucle
284	23	2.3	329	8	ACH19337	Human ova	357	23	2.3	822	6	ABQ44853	Oligonucle
285	23	2.3	330	4	AAL19704	Human bre	358	23	2.3	832	6	ABQ20712	Oligonucle
286	23	2.3	331	5	ABV37589	Human pro	359	23	2.3	832	6	ABQ20712	Oligonucle
287	23	2.3	332	5	ABV37589	Human pro	360	23	2.3	846	6	ABL89819	Human pol
288	23	2.3	333	6	ABL87713	Human ova	361	23	2.3	910	6	ABL89819	Human pol
289	23	2.3	334	6	ACH28792	Human ova	362	23	2.3	918	6	ABN98658	Arabidops
290	23	2.3	335	6	ABL82970	Human ova	363	23	2.3	924	3	AZ57943	Poplar fl
291	23	2.3	336	8	ACH28225	Human adu	364	23	2.3	925	7	AAD49506	Human TRI
292	23	2.3	337	8	AZ07549	Maize glu	365	23	2.3	946	4	AAF85392	Nucleotid
293	23	2.3	338	3	AZ294789	Maize gla	366	23	2.3	946	6	ABK88485	Poplar pr
294	23	2.3	339	3	AAZ76254	Maize glu	367	23	2.3	946	8	ACA62518	Poplar ho
295	23	2.3	340	8	ACH3401	Human foe	368	23	2.3	955	6	AAI69492	A. sulcat
296	23	2.3	341	4	AAF63541	Mushroom	369	23	2.3	961	5	AAS29117	CDNA enco
297	23	2.3	342	8	ACH16144	Human adu	370	23	2.3	961	6	ABG68257	CDNA enco
298	23	2.3	343	8	ACH16144	Human adu	371	23	2.3	961	9	ADC25251	Human CDN
299	23	2.3	344	7	ACC55523	Rice endo	372	23	2.3	1023	3	AAZ22411	Human sec
300	23	2.3	345	8	ACH38046	Human end	373	23	2.3	1093	3	AZ52429	HTRM clon
301	23	2.3	346	7	ACF56800	Rice leaf	374	23	2.3	1112	3	AAZ89463	Rice leud
302	23	2.3	347	8	ACH34768	Human end	375	23	2.3	1161	6	ABQ98641	Human ORF
303	23	2.3	348	4	AAL10124	Human bre	376	23	2.3	1201	6	ADQ06468	Arabidops
304	23	2.3	349	2	AAZ30156	Human sec	377	23	2.3	1206	4	ADQ08312	Human sec
305	23	2.3	350	7	ABZ82360	Rice leaf	378	23	2.3	1210	6	ADQ34112	Human sec
306	23	2.3	351	8	ABV19922	Human pro	379	23	2.3	1213	2	AAT61895	Human 14-
307	23	2.3	352	5	ACH23015	Human adu	380	23	2.3	1213	6	ABK84586	Human CDN
308	23	2.3	353	7	ABX60682	Arabidops	381	23	2.3	1213	9	ADD55777	Thalacres
309	23	2.3	354	4	ADL17973	CDNA (Seq	382	23	2.3	1240	2	AAQ24177	Tox24 gen
310	23	2.3	355	9	ADL17973	CDNA (Seq	383	23	2.3	1241	2	AAV29479	Nucleic a
311	23	2.3	356	7	ABZ73019	Rice leaf	384	23	2.3	1257	5	ADQ07227	Pyenotes
312	23	2.3	357	7	ACF56754	Rice endo	385	23	2.3	1257	6	ABL49613	Apple cin
313	23	2.3	358	3	AAF09443	Fusarium	386	23	2.3	1262	6	ABL49613	Apple cin
314	23	2.3	359	8	ACH33345	Human end	387	23	2.3	1262	8	ADA15454	DNA enco
315	23	2.3	360	9	ABE81415	Arabidops	388	23	2.3	1278	3	AAA54525	Phyryl/pr
316	23	2.3	361	9	ABE81415	Arabidops	389	23	2.3	1278	3	AAA54525	Phyryl/pr

C 535	23	2.3	14708	6	ABL34245	ABL34245 Human imm	C 608	109	5	AAF98685	Aaf98685 Human ova
C 536	23	2.3	14708	6	ABL92325	ABL92325 Chemically	C 609	110	7	ABX53939	Abx53939 Bovine ES
C 537	23	2.3	14708	6	ABK28450	ABK28450 DNA trans	C 610	111	4	AAS07743	Aas07743 Cervical
C 538	23	2.3	15811	4	ABL12090	ABL12090 Drosophila	C 611	112	5	AAB22332	Aab22332 Rat diffe
C 539	23	2.3	15863	9	ABD54166	ABD54166 Pretreat	C 612	113	7	ABX54764	Abx54764 Bovine ES
C 540	23	2.3	15954	6	ABK31494	ABK31494 Signal tr	C 613	114	6	ABV97532	Abv97532 Human pan
C 541	23	2.3	15954	6	ABL70467	ABL70467 Chemically	C 614	115	6	ABL19706	AbL19706 Human bre
C 542	23	2.3	17213	6	ABL33483	ABL33483 Human imm	C 615	116	4	AAF98629	Aaf98629 Human ova
C 543	23	2.3	49999	2	Az223895	Az223895 Murine LO	C 616	117	5	ABV33217	Abv33217 Human pro
C 544	23	2.3	72928	3	Az218355	Az218355 Human AST	C 617	118	5	ABV42140	Abv42140 Human pro
C 545	23	2.3	72928	3	AAAB0253	AAAB0253 Human AST	C 618	119	7	ABX48784	Abx48784 Bovine ES
C 546	23	2.3	73308	6	ABL66966	ABL66966 Lung canc	C 619	120	4	ABL00084	AbL00084 Human rep
C 547	23	2.3	93483	8	ADA03083	ADA03083 Mouse mCG	C 620	121	4	ABL96347	AbL96347 Human tes
C 548	23	2.3	93483	8	ADA66367	ADA66367 Mouse mCG	C 621	122	6	ABK25158	Abk25158 Male-ster
C 549	23	2.3	93483	9	ABD72821	ABD72821 Mouse mCG	C 622	123	6	ABK25157	Abk25157 Male-ster
C 550	22	2.2	27	4	ABX79828	ABX79828 EST polym	C 623	124	5	ABV61528	Abv61528 Human pro
C 551	22	2.2	30	6	ABX89953	ABX89953 PolyA ada	C 624	125	9	ADP35055	Adp35055 Mouse mit
C 552	22	2.2	35	6	ABS64697	ABS64697 Nucleic a	C 625	126	6	ABL86533	AbL86533 Human ova
C 553	22	2.2	35	7	AAV12343	AAV12343 Ribonucle	C 626	127	7	ABX54089	Abx54089 Bovine ES
C 554	22	2.2	37	2	AAV12343	AAV12343 Ribonucle	C 627	128	7	ABX60674	Abx60674 Arabidops
C 555	22	2.2	38	3	Az43892	Az43892 M. tuberc	C 628	129	3	AAZ46504	Aaz46504 Mouse exo
C 556	22	2.2	39	4	AzH20359	AzH20359 HIV6 viru	C 629	130	4	AAZ46504	Aaz46504 Mouse exo
C 557	22	2.2	40	8	ACC83851	ACC83851 Target-sp	C 630	131	6	ABK4612	Abk4612 Human ben
C 558	22	2.2	41	2	AAZ23455	AAZ23455 Human neu	C 631	132	6	ABK4612	Abk4612 Human ben
C 559	22	2.2	41	2	AAZ23455	AAZ23455 Human neu	C 632	133	9	AD61750	Ad61750 Bovine ES
C 560	22	2.2	41	2	AAZ23455	AAZ23455 Human neu	C 633	134	5	ABV05847	Abv05847 Human pro
C 561	22	2.2	43	4	AAZ23455	AAZ23455 Human neu	C 634	135	5	ACD96794	AcD96794 Human col
C 562	22	2.2	43	4	AAZ23455	AAZ23455 Human neu	C 635	136	2	AAZ25911	Aaz25911 Immunod
C 563	22	2.2	44	8	ABD67788	ABD67788 DNA seque	C 636	137	4	ABX55589	Abx55589 Bovine ES
C 564	22	2.2	46	4	AAZ28962	AAZ28962 Human SNP	C 637	138	4	ABX55589	Abx55589 Bovine ES
C 565	22	2.2	47	4	AAZ28962	AAZ28962 Human SNP	C 638	139	4	AAK79568	Aak79568 Human imm
C 566	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 639	140	4	AAK79568	Aak79568 Human imm
C 567	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 640	141	4	AAK79568	Aak79568 Human imm
C 568	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 641	142	4	AAK79568	Aak79568 Human imm
C 569	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 642	143	4	AAK79568	Aak79568 Human imm
C 570	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 643	144	4	AAK79568	Aak79568 Human imm
C 571	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 644	145	4	AAK79568	Aak79568 Human imm
C 572	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 645	146	4	AAK79568	Aak79568 Human imm
C 573	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 646	147	4	AAK79568	Aak79568 Human imm
C 574	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 647	148	4	AAK79568	Aak79568 Human imm
C 575	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 648	149	4	AAK79568	Aak79568 Human imm
C 576	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 649	150	4	AAK79568	Aak79568 Human imm
C 577	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 650	151	4	AAK79568	Aak79568 Human imm
C 578	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 651	152	4	AAK79568	Aak79568 Human imm
C 579	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 652	153	4	AAK79568	Aak79568 Human imm
C 580	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 653	154	4	AAK79568	Aak79568 Human imm
C 581	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 654	155	4	AAK79568	Aak79568 Human imm
C 582	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 655	156	4	AAK79568	Aak79568 Human imm
C 583	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 656	157	4	AAK79568	Aak79568 Human imm
C 584	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 657	158	4	AAK79568	Aak79568 Human imm
C 585	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 658	159	4	AAK79568	Aak79568 Human imm
C 586	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 659	160	4	AAK79568	Aak79568 Human imm
C 587	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 660	161	4	AAK79568	Aak79568 Human imm
C 588	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 661	162	4	AAK79568	Aak79568 Human imm
C 589	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 662	163	4	AAK79568	Aak79568 Human imm
C 590	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 663	164	4	AAK79568	Aak79568 Human imm
C 591	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 664	165	4	AAK79568	Aak79568 Human imm
C 592	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 665	166	4	AAK79568	Aak79568 Human imm
C 593	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 666	167	4	AAK79568	Aak79568 Human imm
C 594	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 667	168	4	AAK79568	Aak79568 Human imm
C 595	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 668	169	4	AAK79568	Aak79568 Human imm
C 596	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 669	170	4	AAK79568	Aak79568 Human imm
C 597	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 670	171	4	AAK79568	Aak79568 Human imm
C 598	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 671	172	4	AAK79568	Aak79568 Human imm
C 599	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 672	173	4	AAK79568	Aak79568 Human imm
C 600	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 673	174	4	AAK79568	Aak79568 Human imm
C 601	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 674	175	4	AAK79568	Aak79568 Human imm
C 602	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 675	176	4	AAK79568	Aak79568 Human imm
C 603	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 676	177	4	AAK79568	Aak79568 Human imm
C 604	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 677	178	4	AAK79568	Aak79568 Human imm
C 605	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 678	179	4	AAK79568	Aak79568 Human imm
C 606	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 679	180	4	AAK79568	Aak79568 Human imm
C 607	22	2.2	51	4	AAZ28962	AAZ28962 Human SNP	C 680	181	4	AAK79568	Aak79568 Human imm

827	22	2.2	248	7	AB273140	Abv73140 Rice leaf	c 900	22	2.2	284	6	ABL62335	Ab162335 Colon ade
828	22	2.2	250	7	ACC60409	Acc60409 Rice leaf	c 901	22	2.2	285	4	AAL16110	Aal16110 Human bre
829	22	2.2	250	8	ACH21509	ACH21509 Human adu	c 902	22	2.2	285	4	AH73173	Ah73173 Human cer
830	22	2.2	251	4	AAK88384	AAK88384 Human dig	903	22	2.2	285	5	ABV49681	Abv49681 Human pro
831	22	2.2	251	4	AAI57596	AAI57596 Human col	904	22	2.2	286	6	ABL86327	Ab186327 Human ova
832	22	2.2	251	6	AB997773	Ab997773 cDNA enco	c 905	22	2.2	286	7	ABX48177	Abx48177 Bovine ES
833	22	2.2	251	9	ADB92853	ADB92853 Human col	906	22	2.2	287	5	ABV18679	Abv18679 Human pro
834	22	2.2	252	5	ABV38113	Abv38113 Human pro	c 907	22	2.2	287	7	ABT22943	Abt22943 Breast ca
835	22	2.2	252	5	ABV05835	Abv05835 Human pro	908	22	2.2	287	7	ABX40723	Abx40723 Bovine ES
836	22	2.2	252	5	ABV58215	Abv58215 Human pro	909	22	2.2	289	2	AAQ53450	AAQ53450 Sequence
837	22	2.2	253	6	ABN95364	ABN95364 Gene #186	910	22	2.2	289	4	AAI88427	Aai88427 Human pol
838	22	2.2	254	4	AAI88770	AAI88770 Human col	911	22	2.2	289	6	AB186581	Ab186581 Human ova
839	22	2.2	254	6	ABU66183	ABU66183 Lung panc	912	22	2.2	291	3	AAA40414	Aaa40414 Pctato in
840	22	2.2	254	6	ABU69715	ABU69715 Prostate	c 913	22	2.2	291	7	ABX36078	Abx36078 Bovine ES
841	22	2.2	254	6	ABK64649	ABK64649 Human ben	c 914	22	2.2	291	7	ABX48529	Abx48529 Bovine ES
842	22	2.2	255	6	ABZ08215	ABZ08215 Human leu	c 915	22	2.2	292	5	ABV60364	Abv60364 Human pro
843	22	2.2	255	7	ABX40562	Abx40562 Bovine ES	c 916	22	2.2	293	6	ABV96589	Abv96589 Human pan
844	22	2.2	256	5	ABV52378	Abv52378 Human pro	917	22	2.2	293	6	ABV47666	Abv47666 Human pro
845	22	2.2	256	7	ABX44248	Abx44248 Bovine ES	c 918	22	2.2	294	6	ABV98318	Abv98318 Human pan
846	22	2.2	257	5	ABV59128	Abv59128 Human pro	c 919	22	2.2	295	4	AAH71373	Aah71373 Human cer
847	22	2.2	258	4	AAK76443	AAK76443 Human imm	c 920	22	2.2	296	4	AAL21959	Aal21959 Human bre
848	22	2.2	258	5	AAV37311	AAV37311 Human pro	921	22	2.2	296	4	AAL09995	Aal09995 Human bre
849	22	2.2	258	6	ABV98312	Abv98312 Human pan	922	22	2.2	296	4	AAL19575	Aal19575 Human bre
850	22	2.2	259	7	ABX38288	Abx38288 Bovine ES	923	22	2.2	296	8	ACC73218	Acc73218 Cat flea
851	22	2.2	259	7	ABX42068	Abx42068 Bovine ES	924	22	2.2	297	5	ABV47069	Abv47069 Human pro
852	22	2.2	260	5	ABV43376	Abv43376 Human pro	925	22	2.2	297	5	ABV48217	Abv48217 Human pro
853	22	2.2	260	5	ABV34518	Abv34518 Human pro	926	22	2.2	299	5	ABX38466	Abx38466 Bovine ES
854	22	2.2	261	4	AAL13658	Aal13658 Human bre	c 927	22	2.2	299	7	ABX43610	Abx43610 Bovine ES
855	22	2.2	261	4	AAH69973	AAH69973 Human cer	c 928	22	2.2	300	7	ABX41086	Abx41086 Bovine ES
856	22	2.2	261	5	ABU43437	ABU43437 Human pro	929	22	2.2	301	4	AAH72063	Aah72063 Human cer
857	22	2.2	261	6	ABU87207	ABU87207 Human ova	930	22	2.2	301	5	ABV19472	Abv19472 Human pro
858	22	2.2	262	7	ABX50456	Abx50456 Bovine ES	931	22	2.2	302	5	ABV48358	Abv48358 Human pro
859	22	2.2	262	7	AAL13089	Aal13089 Human bre	932	22	2.2	302	5	ABV49607	Abv49607 Human pro
860	22	2.2	266	5	ABV16092	Abv16092 Human pro	933	22	2.2	302	7	ABX36938	Abx36938 Bovine ES
861	22	2.2	266	5	ABV39058	Abv39058 Human pro	934	22	2.2	303	4	AAQ525408	AAQ525408 Human ova
862	22	2.2	267	5	ABV05178	ABV05178 Human pro	c 935	22	2.2	303	7	ABX60984	Abx60984 Arabidops
863	22	2.2	267	6	ABU85849	ABU85849 Human ova	936	22	2.2	304	5	ABV19428	Abv19428 Human pro
864	22	2.2	267	6	ABU85885	ABU85885 Human ova	937	22	2.2	305	4	AAH70485	Aah70485 Human cer
865	22	2.2	268	4	AAK79559	AAK79559 Human imm	938	22	2.2	305	5	ABV58043	Abv58043 Human pro
866	22	2.2	268	5	ABV38724	Abv38724 Human pro	c 939	22	2.2	305	5	ABV14717	Abv14717 Human pro
867	22	2.2	268	8	ACD10979	ACD10979 Human col	940	22	2.2	306	3	AAA70249	Aaa70249 Plasmodiu
868	22	2.2	268	8	ABX46302	Abx46302 Bovine ES	941	22	2.2	306	5	ABV48259	Abv48259 Human pro
869	22	2.2	269	4	AAK79558	AAK79558 Human imm	c 942	22	2.2	306	5	ABV04231	Abv04231 Human pro
870	22	2.2	269	5	ABV16341	ABV16341 Human pro	c 943	22	2.2	306	5	ABV05548	Abv05548 Human pro
871	22	2.2	272	4	AAL12612	Aal12612 Human bre	c 944	22	2.2	307	6	ABU87642	Abu87642 Human ova
872	22	2.2	272	4	AAK61195	AAK61195 Human imm	c 945	22	2.2	310	6	ABL87211	Ab187211 Human ova
873	22	2.2	272	6	ABX98906	Abx98906 DNA of pl	c 946	22	2.2	311	6	ABL87180	Ab187180 Human ova
874	22	2.2	272	7	ABX41821	Abx41821 Bovine ES	947	22	2.2	312	4	AAK57869	Aak57869 Human imm
875	22	2.2	273	3	AAQ55668	AAQ55668 Human dif	c 948	22	2.2	312	7	ABX47010	Abx47010 Bovine ES
876	22	2.2	273	4	AAH69948	AAH69948 Human cer	949	22	2.2	312	7	ABX43249	Abx43249 Bovine ES
877	22	2.2	273	7	ACF03923	ACF03923 Rice endo	c 950	22	2.2	312	7	ABZ17927	Abz17927 S2 subtra
878	22	2.2	273	8	ACD81660	ACD81660 Human des	951	22	2.2	313	2	AAV09110	Aav09110 3' nucleot
879	22	2.2	274	5	ABV58263	Abv58263 Human pro	952	22	2.2	313	2	AAH77541	Aah77541 Murine se
880	22	2.2	274	6	ABZ08581	ABZ08581 Human leu	c 953	22	2.2	313	3	AAZ59483	Aaz59483 Murine se
881	22	2.2	275	5	ABV61335	Abv61335 Human pro	c 954	22	2.2	313	4	AAL19798	Aal19798 Human bre
882	22	2.2	275	5	ABV57365	Abv57365 Human pro	c 955	22	2.2	313	4	AAL13719	Aal13719 Human bre
883	22	2.2	277	5	ABV49364	Abv49364 Human pro	956	22	2.2	313	9	ADC38798	Adc38798 Human cDN
884	22	2.2	277	7	ABX47508	Abx47508 Bovine ES	c 957	22	2.2	314	6	AB163852	Ab163852 Breast ca
885	22	2.2	277	7	ABX47508	Abx47508 Bovine ES	c 958	22	2.2	314	5	ABV19372	Abv19372 Human pro
886	22	2.2	278	4	AAH69999	AAH69999 Human cer	c 959	22	2.2	316	5	ABV08599	Abv08599 Human pro
887	22	2.2	280	4	AAK86795	AAK86795 Human imm	c 960	22	2.2	317	4	AAL13715	Aal13715 Human bre
888	22	2.2	280	4	AAK85223	AAK85223 Human imm	961	22	2.2	317	7	ABX39797	Abx39797 Bovine ES
889	22	2.2	280	5	ABZ21126	ABZ21126 Human ner	c 962	22	2.2	318	2	AAQ59920	AAQ59920 Human bra
890	22	2.2	280	5	ABV58623	Abv58623 Human pro	963	22	2.2	318	5	ABV49219	Abv49219 Human pro
891	22	2.2	281	4	AAL17457	Aal17457 Human bre	964	22	2.2	318	5	ABV56059	Abv56059 Human pro
892	22	2.2	281	7	ABV50616	ABV50616 Bovine ES	c 965	22	2.2	318	6	AB161862	Ab161862 Colon ade
893	22	2.2	282	2	AAZ20011	AAZ20011 Spider ve	c 966	22	2.2	318	7	ABX55820	Abx55820 Bovine ES
894	22	2.2	282	2	AAZ20006	AAZ20006 Spider ve	967	22	2.2	319	5	ABV58473	Abv58473 Human pro
895	22	2.2	282	4	AAL20269	Aal20269 Human bre	968	22	2.2	320	4	AAK88435	Aak88435 Human dig
896	22	2.2	282	5	ABV47775	ABV47775 Human pro	969	22	2.2	320	5	AAQ59536	Aaq59536 cDNA enco
897	22	2.2	283	7	ABX35652	Abx35652 Bovine ES	970	22	2.2	320	7	ABX49272	Abx49272 Bovine ES
898	22	2.2	283	7	ABX35067	ABX35067 Bovine ES	971	22	2.2	320	8	ABD32262	Abd32262 Human rox
899	22	2.2	284	5	ABV04489	ABV04489 Human pro	972	22	2.2	321	6	ABN18364	Abn18364 Human ORF

CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention

XX Sequence 121 BP; 20 A; 36 C; 40 G; 25 T; 0 U; 0 Other;
 SQ Query Match 2.7%; Score 27; DB 6; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ACCAACAGGCGAGTGACTTCTCCAAAG 69
 DB 106 ACCAACAGGCGAGTGACTTCTCCAAAG 80

RESULT 4

ABK25241
 ID ABK25241 standard; DNA; 121 BP.

XX AC ABK25241;

XX DT 09-APR-2002 (first entry)

XX DE Male-sterile plant producing genome altering oligonucleotide #141.

XX KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 KW o-methyl modification; LNA modification; phosphorothioate linkage;
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
 KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
 KW amino acid over production; herbicide resistance; glyphosate resistance;
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;
 KW modified oil production; modified starch production; waxy starch;
 KW altered floral morphology; male-sterile plant; albino mutant;
 KW increased stearate production; reduced palmitate production; albino plant;
 KW photosynthetic process.

XX OS Triticum aestivum.

XX OS Synthetic.

XX PN WO200192512-A2.

XX PD 06-DEC-2001.

XX PF 01-JUN-2001; 2001WO-US017672.

XX PR 01-JUN-2000; 2000US-0208538P.

XX PR 30-OCT-2000; 2000US-0244989P.

XX PR 27-MAR-2001; 2001US-00818875.

XX PA (UYDE) UNIV DELAWARE.

XX PI Kmiec EB, Gamper HB, Rice MC, Kim J;

XX DR WPI; 2002-106307/14.

XX PT New oligonucleotides with modified nuclease-resistant termini, useful for

PT creating plants with desired phenotypes, e.g. stress tolerance, improved
 PT nutritional value, herbicide or disease resistance, or modified oil
 PT production.

XX Claim 7; Page 79; 220pp; English.

XX CC The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain. The DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises
 CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention

XX SQ Sequence 121 BP; 25 A; 40 C; 36 G; 20 T; 0 U; 0 Other;

Query Match 2.7%; Score 27; DB 6; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.36;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ACCAACAGGCGAGTGACTTCTCCAAAG 69

DB 16 ACCAACAGGCGAGTGACTTCTCCAAAG 42

RESULT 5

ABK25237

ID ABK25237 standard; DNA; 121 BP.

XX AC ABK25237;

XX DT 09-APR-2002 (first entry)

XX DE Male-sterile plant producing genome altering oligonucleotide #137.

XX KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 KW o-methyl modification; LNA modification; phosphorothioate linkage;
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
 KW abiotic stress tolerance; improved nutritional value; hygromycin-B;
 KW amino acid over production; herbicide resistance; glyphosate resistance;
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;
 KW modified oil production; modified starch production; waxy starch;
 KW altered floral morphology; male-sterile plant; albino mutant;
 KW increased stearate production; reduced palmitate production; albino plant;
 KW photosynthetic process.

XX OS Triticum aestivum.

XX OS Synthetic.

XX PN WO200192512-A2.

XX PD 06-DEC-2001.

XX PF 01-JUN-2001; 2001WO-US017672.

XX PR 01-JUN-2000; 2000US-0208538P.


```
PR 30-OCT-2000; 2000US-0244989P.
PR 27-MAR-2001; 2001US-00818875.
XX (UYDE ) UNIV DELAWARE.
XX Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful for
XX creating plants with desired phenotypes, e.g. stress tolerance, improved
XX nutritional value, herbicide or disease resistance, or modified oil
XX production.
XX Claim 7; Page 79; 220pp; English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
XX genetic sequence, which comprises a single-stranded oligonucleotide
XX having a DNA domain. The DNA domain has at least one mismatch with
XX respect to the genetic sequence to be altered and further comprises
XX chemical modifications of the oligonucleotide. The chemical modifications
XX consist of o-methyl modification, an LNA modification, two or more
XX phosphorothioate linkages on a terminus, or a combination of any two or
XX more of these modifications. The oligonucleotides are useful for
XX directing repair or alteration of plant genetic information. The
XX oligonucleotides are particularly useful for creating plants with desired
XX phenotypes, e.g. environmental or abiotic stress tolerance, improved
XX nutritional value (e.g. altering amino acid content of plants or
XX conferring amino acid over production), herbicide resistance (e.g.
XX glyphosate resistance, imidazolinone and sulphonylurea herbicide
XX resistance, porphyrin herbicide resistance or triazine resistance),
XX disease resistance, modified oil production, modified starch production
XX (e.g. increased starch or production of waxy starch), altered floral
XX morphology (e.g. male-sterile plants) or modified fatty acid content
XX (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
XX The oligonucleotides are also useful for producing albino mutants for the
XX analysis of photosynthetic processes. This sequence represents a genome
XX altering oligonucleotide of the invention
XX
XX Sequence 121 BP; 31 A; 35 C; 38 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 2.7%; Score 27; DB 6; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 0.36;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 43 ACCACAGGCGAGGTGACCTACTCCAAAG 69
XX |||||
XX Db 27 ACCACAGGCGAGGTGACCTACTCCAAAG 53
XX
XX RESULT 6
XX ABK25238/C
XX -ID ABK25238 standard; DNA; 121 BP.
XX
XX AC ABK25238;
XX
XX XX 09-APR-2002 (first entry)
XX
XX DE Male-sterile plant producing genome altering oligonucleotide #138.
XX
XX KW Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
XX o-methyl modification; LNA modification; phosphorothioate linkage;
XX DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
XX abiotic stress tolerance; improved nutritional value; hygromycin-B;
XX amino acid over production; herbicide resistance; glyphosate resistance;
XX imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
XX porphyrin herbicide resistance; triazine resistance; disease resistance;
XX modified oil production; modified starch production; waxy starch;
XX altered floral morphology; male-sterile plant; albino mutant;
XX modified fatty acid content; reduced palmitate production; albino plant;
XX increased stearate production; reduced linolenic acid production;
XX photosynthetic process.
XX
OS Triticum aestivum.
OS Synthetic.
XX PN W0200192512-A2.
XX PD 06-DEC-2001.
XX PF 01-JUN-2001; 2001WO-US017672.
XX PR 01-JUN-2000; 2000US-0208538P.
XX PR 30-OCT-2000; 2000US-0244989P.
XX PR 27-MAR-2001; 2001US-00818875.
XX PA (UYDE ) UNIV DELAWARE.
XX PI Kmiec EB, Gamper HB, Rice MC, Kim J;
XX WPI; 2002-106307/14.
XX
XX New oligonucleotides with modified nuclease-resistant termini, useful for
XX creating plants with desired phenotypes, e.g. stress tolerance, improved
XX nutritional value, herbicide or disease resistance, or modified oil
XX production.
XX Claim 7; Page 79; 220pp; English.
XX
XX The invention relates to an oligonucleotide for targeted alteration of a
XX genetic sequence, which comprises a single-stranded oligonucleotide
XX having a DNA domain. The DNA domain has at least one mismatch with
XX respect to the genetic sequence to be altered and further comprises
XX chemical modifications of the oligonucleotide. The chemical modifications
XX consist of o-methyl modification, an LNA modification, two or more
XX phosphorothioate linkages on a terminus, or a combination of any two or
XX more of these modifications. The oligonucleotides are useful for
XX directing repair or alteration of plant genetic information. The
XX oligonucleotides are particularly useful for creating plants with desired
XX phenotypes, e.g. environmental or abiotic stress tolerance, improved
XX nutritional value (e.g. altering amino acid content of plants or
XX conferring amino acid over production), herbicide resistance (e.g.
XX glyphosate resistance, imidazolinone and sulphonylurea herbicide
XX resistance, porphyrin herbicide resistance or triazine resistance),
XX disease resistance, modified oil production, modified starch production
XX (e.g. increased starch or production of waxy starch), altered floral
XX morphology (e.g. male-sterile plants) or modified fatty acid content
XX (e.g. reduced palmitate, increased stearate or reduced linolenic acid).
XX The oligonucleotides are also useful for producing albino mutants for the
XX analysis of photosynthetic processes. This sequence represents a genome
XX altering oligonucleotide of the invention
XX
XX Sequence 121 BP; 17 A; 38 C; 35 G; 31 T; 0 U; 0 Other;
XX
XX Query Match 2.7%; Score 27; DB 6; Length 121;
XX Best Local Similarity 100.0%; Pred. No. 0.36;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 43 ACCACAGGCGAGGTGACCTACTCCAAAG 69
XX |||||
XX Db 95 ACCACAGGCGAGGTGACCTACTCCAAAG 69
XX
XX RESULT 7
XX ACH38095
XX -ID ACH38095 standard; cDNA; 390 BP.
XX
XX AC ACH38095;
XX
XX DT 13-OCT-2003 (first entry)
XX
XX DE Human endothelial cell cDNA #6228.
XX
XX KW Human; ss; sequencing by hybridisation; SSH; expressed sequence tag; EST;
XX genome mapping; biodiversity; genetic disorder.
XX
```


KW Arabidopsis thaliana; insecticide; fungicide; plant; mapping; diagnosis;
KW Genetic modification; gene; ss.
OS Arabidopsis thaliana.
XX US2002023280-A1.
FN 21-FEB-2002.
XX 26-JAN-2001; 2001US-00770444.
XX 27-JAN-2000; 2000US-0178502P.
XX (GORLACH J.
PA (ANY) AN Y.
PA (HAMI) HAMILTON C M.
PA (PRIC) PRICE J L.
PA (RAIN) RAINES T M.
PA (YUY) YU Y.
PA (RAME) RAMEAKA J G.
PA (PAGE) PAGE A.
PA (MATH) MATHW A V.
PA (LEDF) LEDFORD B L.
PA (WOES) WOESSNER J P.
PA (HAAS) HAAS W D.
PA (GARC) GARCIA C A.
PA (KRIC) KRICKER M.
PA (SLAT) SLATER T.
PA (DAVI) DAVIS K R.
PA (ALLE) ALLEN K.
PA (HOFF) HOFFMAN N.
PA (HURB) HURBAN P.
XX Goralach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX WPI; 2002-267486/31.
XX New Arabidopsis thaliana nucleic acid, for identifying homologous genes,
PT producing compositions that modulate the expression or function of its
PT encoded protein, and mapping functional regions of a protein.
XX Claim 1; SEQ ID NO 474; 44pp; English.
XX The present invention describes an Arabidopsis thaliana nucleic acid (I)
CC comprising a sequence capable of hybridizing under stringent conditions
CC to a sequence (S1) selected from any one of the 999 sequences given in
CC ABL93236 to ABL94234. (I) have insecticide and fungicide activities, and
CC they can be used as protein expression modulators. (I) can be used in
CC identifying homologous or related genes, in producing compositions that
CC modulate the expression or function of their encoded proteins, mapping
CC functional regions of the proteins, and in studying associated
CC physiological pathways. (I) can also be used: (1) for the genetic
CC manipulation of cells, particularly plant cells; (2) in screening assays
CC of various plant strains to determine the strains that are best capable
CC of withstanding a particular disease or environmental stress; (3) for
CC enhancing or inhibiting production of a biosynthetic product in a plant;
CC (4) as probes in mapping and in diagnosis, in genetic modification and
CC for screening purposes, to generate additional copies of the nucleic
CC acids, to generate ribozymes or antisense oligonucleotides, and as single
CC -stranded DNA probes or as triple-strand forming oligonucleotides; and (5)
CC for generating genetically modified transgenic organisms. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO web site
XX SQ Sequence 458 BP; 131 A; 71 C; 74 G; 182 T; 0 U; 0 Other;
Query Match 2.7%; Score 27; DB 6; Length 458;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TTTTGATATAAAAAAAAAAAAAAAAAAAAAA 982
DB 82 TTTTGATATAAAAAAAAAAAAAAAAAAAAAA 56

RESULT 10

ABQ65619/C
ID ABQ65619 standard; DNA; 712 BP.

XX AC ABQ65619;

XX 21-AUG-2002 (first entry)

XX Arabidopsis thaliana polynucleotide SEQ ID NO 196.

XX Arabidopsis thaliana; thale cress; plant; transgenic; GMO; disease;
KW stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide;
KW insecticide; antibiotic; ds.

XX Arabidopsis thaliana.

XX US2002059663-A1.

XX 16-MAY-2002.

XX 26-JAN-2001; 2001US-00770149.

XX 27-JAN-2000; 2000US-0178506P.

XX (GORLACH J.
PA (ANY) AN Y.
PA (HAMI) HAMILTON C M.
PA (PRIC) PRICE J L.
PA (RAIN) RAINES T M.
PA (YUY) YU Y.
PA (RAME) RAMEAKA J G.
PA (PAGE) PAGE A.
PA (MATH) MATHW A V.
PA (LEDF) LEDFORD B L.
PA (WOES) WOESSNER J P.
PA (HAAS) HAAS W D.
PA (GARC) GARCIA C A.
PA (KRIC) KRICKER M.
PA (SLAT) SLATER T.
PA (DAVI) DAVIS K R.
PA (ALLE) ALLEN K.
PA (HOFF) HOFFMAN N.
PA (HURB) HURBAN P.

Goralach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
Hurban P;

WPI; 2002-479224/51.

New nucleic acid that hybridizes to Arabidopsis thaliana sequences,
useful e.g. for preparing transgenic plants with increased resistance or
altered metabolism.

Claim 1; SEQ ID NO 196; 40pp + Sequence Listing; English.

The invention relates to nucleic acids (I) that hybridize under stringent
conditions to any of 999 sequences (ABQ65424-ABQ66422) or their
fragments. (I) are used to express the corresponding polypeptides (II) or
to produce genetically modified plant cells or transgenic plants, which
may have improved resistance to disease or stress, or altered
metabolic/biosynthetic pathways (for production of commercial,
nutritional or medicinal products), or generally any trait of interest,
or can be used to screen for biologically active agents (e.g. fungicides,
insecticides and antibiotics). Note: The sequence data for this patent
did not form part of the printed specification, but was obtained in

CC electronic format directly from the USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=99909770149

XX Sequence 712 BP; 198 A; 194 C; 132 G; 188 T; 0 U; 0 Other;

Query Match 2.7%; Score 27; DB 6; Length 712;
 Best Local Similarity 100.0%; Pred. No. 0.28;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 955 CTTTGTATATAAAAAAAAAAAAAAAAAAAAA 981
 DB 28 CTTTGTATATAAAAAAAAAAAAAAAAAAAAA 2

RESULT 11

AAD06338
 ID AAD06338 standard; cDNA; 980 BP.

XX AAD06338;

DT 06-AUG-2003 (revised)

DT 10-AUG-2001 (first entry)

DE Pentaclethra macroloba partial lipid acyl hydrolase (LAH) cDNA.

KW Pentin-1; lipid acyl hydrolase; LAH; gene shuffling; insecticidal;
 KW pathogenic infection; pest; transgenic plant; insect infestation;
 KW genetic manipulation; agricultural crop; ss.

XX Pentaclethra macroloba.

XX Key Location/Qualifiers
 FH CDS 1..828

FT /tag= a
 FT /product= "Lipid acyl hydrolase (LAH) protein"
 FT /note= "Does not include start codon"
 FT /partial

PN WO200136468-A2.

PD 25-MAY-2001.

PF 15-NOV-2000; 2000WO-US031408.

PR 15-NOV-1999; 99US-0165455P.

PA (PION-) PIONEER HI-BRED INT INC.

PI Cigan AL;

XX WPI; 2001-355613/37.

DR P-PSDB; AAE02392.

PT New nucleic acid encoding lipid acyl hydrolase proteins having pesticidal
 PT activity, derived from rice, soybean, or wheat, for controlling insect
 PT infestation and pathogenic infection in transgenic plants.

PS Claim 1; Fig 7; 89pp; English.

XX The invention relates to Pentin-1-like lipid acyl hydrolases (LAH) and
 CC their corresponding cDNA molecules. LAH is useful for controlling insect
 CC infestation and pathogenic infections in transgenic plants. LAH cDNA
 CC confers pesticidal resistance to organisms into which it has been
 CC introduced and is also useful in mutagenic and recombinogenic protocols,
 CC to produce polypeptides with improved biological activities. LAH cDNA is
 CC also useful in the genetic manipulation of plants and for transforming
 CC bacteria, fungi, yeast and other organisms. LAH having pesticidal
 CC activity is useful for protecting plants, in particular agricultural
 CC crops from pests, including insects, fungi, bacteria, nematodes, viruses
 CC or viroids and in particular insect pests. LAH cDNA is further useful in
 CC gene shuffling protocols for generating libraries of polynucleotides
 CC having a desired characteristic. LAH can be used alone or in combination
 CC with other proteins or agents from Bacillus, including delta-endotoxin

CC and vegetative insecticidal proteins, protease inhibitors, lectins, alpha
 CC -amylases, peroxidases and cholesterol oxidase, to control different
 CC insect pests. The present cDNA sequence encodes partial Pentaclethra
 CC lipid acyl hydrolase (LAH) protein. (Updated on 06-AUG-2003 to correct OS
 CC field.)

XX Sequence 980 BP; 341 A; 177 C; 197 G; 265 T; 0 U; 0 Other;

Query Match 2.7%; Score 27; DB 4; Length 980;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 954 GCTTTTGATATAAAAAAAAAAAAAAAAAAAAA 980

DB 954 GCTTTTGATATAAAAAAAAAAAAAAAAAAAAA 980

RESULT 12

AAT66687

ID AAT66687 standard; cDNA; 1167 BP.

XX AAT66687;

DT 17-OCT-2003 (revised)

DT 25-JUL-1997 (first entry)

XX Soybean peroxidase SEPB2 cDNA.

DE Peroxidase; SEPB2; soybean; plant breeding; pulp; paper; bleaching;
 KW waste disposal; soil reclamation; remediation; monoclonal antibody; ss.

XX Glycine max; cv. Resnik.

XX Key Location/Qualifiers
 FH CDS 39..980

FT /tag= a

FT sig_peptide 39..101

FT /tag= b

FT mat_peptide 102..977

FT /tag= c

FT polyA_signal 1126..1130

FT /tag= d

PN WO9715656-A1.

XX 01-MAY-1997.

PF 11-OCT-1996; 96WO-US016354.

PR 27-OCT-1995; 95US-00549658.

PA (INDI-) INDIANA CROP IMPROVEMENT ASSOC.

PI Vierling RA;

XX WPI; 1997-259011/23.

DR P-PSDB; AAW16610.

PT Isolated soybean peroxidase genes - useful for developing products for
 PT quantification and monitoring of peroxidase activity.

PS Claim 16; Page 43-44; 63pp; English.

XX cDNA clones (AAT66684-87) respectively code for soybean peroxidases
 CC SEPA1, SEPB2, SEPB1 and SEPB2 (AAW16607-10). Plant peroxidase specific
 CC primer PSP (AAT66679) was generated from the conserved distal haem ligand
 CC (AAW16603) in all plant peroxidases, and was used to generate a
 CC peroxidase gene probe. Primary hybridisation screening using the probe
 CC yielded 25 clones. 11 Positive clones were recovered after 2 rounds of
 CC PCR using PSP and a T7 vector primer, and 4 clones, SEPA1, SEPB2, SEPB1
 CC and SEPB2, were further analysed. The soybean peroxidase genes can be
 CC used to develop products for the quantification and monitoring of
 CC peroxidase activity, e.g. in assays such as ELISA, PCR, plant breeding

CC programmes, pulp and paper bleaching, on-site waste destruction, soil
CC remediation and organic synthesis. (Updated on 17-OCT-2003 to standardise
CC OS field)

SQ Sequence 1167 BP; 385 A; 232 C; 231 G; 319 T; 0 U; 0 Other;
Query Match 2.7%; Score 27; DB 2; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 956 TTTTGATATAAAAAAAAAAAAAAAAAAAAA 982
Db 1139 TTTTGATATAAAAAAAAAAAAAAAAAAAAA 1165

RESULT 13
AAV69276
ID AAV69276 standard; cDNA; 1167 BP.
XX AC
XX AAV69276;
XX 29-JAN-1999 (first entry)
XX Soybean peroxidase SEPB2 polypeptide encoding cDNA.
DE Soybean peroxidase; SEPal; SEPa2; SEPB1; SEPB2; recombinant; industry;
KW diagnostic chemistry; ss.
XX Glycine max.

Key Location/Qualifiers
FH 5'UTR 1..38
FT /*tag= a
FT CDS 39..980
FT /*tag= b
FT /product= "SEPB2 polypeptide"
FT sig_peptide 39..101
FT /*tag= c
FT mat_peptide 102..977
FT /*tag= d
FT 3'UTR 978..1167
FT /*tag= e

XX US5840558-A.
XX 24-NOV-1998.
XX 27-OCT-1995; 95US-00671320.
XX 27-OCT-1995; 95US-00671320.
XX (INDI-) INDIANA CROP IMPROVEMENT ASSOC.

XX Vierling RA;
XX WPI; 1999-034041/03.
XX P-PSDB; AAW81496.
XX cDNA encoding soya peroxidase SEPal - useful for producing recombinant
XX peroxidase.
XX Example 7; Col 35-38; 31pp; English.
XX This cDNA encodes a soybean peroxidase SEPB2 polypeptide. The invention
XX provides four cDNA sequences (AAV69273 to AAV69276) encoding soybean
XX peroxidases SEPal, SEPa2, SEPB1 and SEPB2 (AAW81493 to AAW81496)
XX respectively. An expression vector containing the SEPal cDNA sequence can
XX be used to transform host cells for the recombinant production of the
XX peroxidase. The peroxidase is useful in industries and diagnostic
XX chemistries

XX SQ Sequence 1167 BP; 385 A; 232 C; 231 G; 319 T; 0 U; 0 Other;

Query Match 2.7%; Score 27; DB 2; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 956 TTTTGATATAAAAAAAAAAAAAAAAAAAAA 982
Db 1139 TTTTGATATAAAAAAAAAAAAAAAAAAAAA 1165

RESULT 14
AAV81423
ID AAV81423 standard; cDNA; 1167 BP.
XX AC
XX AAV81423;
XX 12-APR-1999 (first entry)
XX Soybean peroxidase SEPB2 cDNA.
DE Peroxidase; SEPB2; soybean; transgenic plant; immunoassay; assay; pulp;
KW paper; bleaching; bioremediation; soil decontamination; ss.
XX Glycine max.

Key Location/Qualifiers
FH CDS 39..980
FT /*tag= a
FT sig_peptide 39..101
FT /*tag= b
FT mat_peptide 102..977
FT /*tag= c
FT polyA_signal 1126..1131
FT /*tag= d

XX WO9855629-A2.
XX 10-DEC-1998.
XX 04-JUN-1998; 98WO-US011421.
XX 04-JUN-1997; 97US-00868577.
XX (INDI-) INDIANA CROP IMPROVEMENT ASSOC.

XX Vierling RA;
XX WPI; 1999-070273/06.
XX P-PSDB; AAW67734.
XX New soybean peroxidase genes - useful, e.g. in pulp and paper bleaching,
XX on site waste destruction and soil remediation.
XX Example 8; Page 48-49; 78pp; English.

XX This cDNA clone codes for novel soybean peroxidase SEPB2 (see AAW67734).
XX 4 Clones, designated SEPal, SEPa2, SEPB1 and SEPB2 (see AAV81420-23) were
XX isolated from a soybean cv. Resnick seedling cDNA library using a plant
XX peroxidase specific primer (see AAV81424) and 3'RACE. Genomic clones (see
XX AAV81418-19) for SEPal and SEPB1 were also obtained. The coding regions of
XX SEPal and SEPB2 exhibit 97% amino acid identity, the coding regions of
XX SEPB1 and SEPB2 share 95% amino acid identity, and the coding regions of
XX SEPal and SEPB1 share 47% amino acid identity. The peroxidases are useful
XX in pulp and paper bleaching, on-site waste destruction, soil remediation,
XX organic synthesis and diagnostic chemistries. Soybean peroxidase has
XX advantages over chlorine bleach, being cheaper, more environmentally
XX friendly, and producing hydroxyl ions with twice the oxidising power of
XX chlorine ions. The plant enzyme is cheap and easy to produce. The
XX invention also relates to immunoassays or oligonucleotide assays which
XX utilise soybean peroxidase as marker

XX SQ Sequence 1167 BP; 385 A; 232 C; 231 G; 319 T; 0 U; 0 Other;

Query Match 2.7%; Score 27; DB 2; Length 1167;

Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TTTTGATATAAAAAAAAAAAAAAAAAA 982
|||||

Dd 1139 TTTTGATATAAAAAAAAAAAAAAAAAA 1165

Search completed: September 25, 2004, 22:56:21
Job time : 505.966 secs

RESULT 15
ADA01011
ID ADA01011 standard; cDNA; 1167 BP.
XX
XX
ADA01011;
AC
XX
XX
06-NOV-2003 (first entry)
DT
DT
XX
XX
cDNA encoding soybean peroxidase GmEPb2.
DE
DE
XX
XX
Soybean peroxidase; gene promoter; transgenic plant; peroxidase activity;
KW plant; GmEPb2; gene; ss.
KW
XX
XX
Glycine max.
OS

PH	Key	Location/Qualifiers
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FT		39..980
FT	CDS	/*tag= c
FT		/product= "GmEPb2"
FT	sig_peptide	39..101
FT		/*tag= b
FT	mat_peptide	102..977
FT		/*tag= d
FT	3'UTR	981..1167
FT		/*tag= e
XX		
XX	US6586583-B1.	
XX		
XX	01-JUL-2003.	
XX		
XX	09-DEC-1998;	98US-00207914.
XX		
XX	27-OCT-1995;	95US-00671320.
XX	04-JUN-1997;	97US-00868577.
XX		
XX	(INDI-) INDIANA CROP IMPROVEMENT ASSOC.	

New recombinant DNA molecule, useful for producing transgenic plants, including transgenic soybeans and in immunoassays or oligonucleotide assays that utilize soybean peroxidase as a marker.

Example 7; Col 61-64; 85pp; English.

The present invention relates to soybean peroxidase genomic DNA and gene promoters for producing transgenic plants, including soybean transgenic plants. The invention also relates to immunoassays or oligonucleotide assays which employ soybean peroxidase as a marker for peroxidase activity. The present sequence encodes soybean peroxidase GmPpB2.

Sequence 1167 BP; 385 A; 232 C; 231 G; 319 T; 0 U; 0 Other;

Query Match	2.7%;	Score 27;	DB 8;	Length 1167;
Best Local Similarity	100.0%;	Pred. No. 0.26;		
Matches 27;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

DY 956 TTTTGATAAAAAAAAAAAAAA 982
||| ||| ||| ||| ||| ||| ||| |||
Db 1139 TTTTGATAAAAAAAAAAAAAA 1165

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 25, 2004, 22:22:22 ; Search time 85.9913 Seconds
(without alignments)
6337.402 Million cell updates/sec

Title: US-10-069-527-3

Perfect score: 982

Sequence: 1 atggcgcggaagattga.....aaaaaaaaaaaaaaaaaaaaa 982

Scoring table: OLIGO NUC

Gapop 50.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents NA: *

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- 4: /cgn2_6/ptodata/2/ina/6B COMB.seq: *
- 5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq: *
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	27	2.7	1167	2	US-08-868-577-16
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4	26	2.6	1154	3	US-08-651-136C-7
5	26	2.6	1154	4	US-09-229-911A-7
6	26	2.6	1378	6	5188642-3
c 7	25	2.5	396	4	US-09-640-173-77
c 8	25	2.5	396	4	US-09-713-550-77
9	25	2.5	1146	3	US-08-893-654B-5
10	25	2.5	1402	3	US-09-196-520-5
11	25	2.5	1940	1	US-08-429-742-3
12	25	2.5	4134	4	US-09-162-021B-1
13	25	2.5	4134	4	US-09-687-477-17
14	25	2.5	4134	4	US-09-687-476-17
15	25	2.5	4134	4	US-09-687-372-17
16	25	2.5	4134	4	US-09-975-553-17
17	25	2.5	4134	4	US-10-270-795-17
18	25	2.5	4134	4	US-10-270-876-17
19	24	2.4	47	4	US-09-453-190B-12
20	24	2.4	47	4	US-09-619-103-10
21	24	2.4	64	1	US-08-055-390-10
22	24	2.4	595	3	US-09-385-982-276
23	24	2.4	923	3	US-09-004-731-66
24	24	2.4	923	3	US-08-749-699-66
25	24	2.4	923	4	US-09-004-729-66
26	24	2.4	1133	4	US-09-395-674B-5
27	24	2.4	1305	4	US-08-815-783-3

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31	24	2.4	1607	2	US-08-986-217-4	Sequence 4, Appli
32	24	2.4	1624	3	US-08-582-740-67	Sequence 67, Appli
33	24	2.4	1624	3	US-09-109-879-67	Sequence 67, Appli
34	24	2.4	1734	4	US-08-630-915A-23	Sequence 23, Appli
35	24	2.4	1921	4	US-09-057-996-7	Sequence 7, Appli
36	24	2.4	1971	2	US-08-892-770-4	Sequence 4, Appli
37	24	2.4	2187	4	US-09-127-219B-2	Sequence 2, Appli
c 38	23	2.3	40	3	US-09-306-290-22	Sequence 22, Appli
39	23	2.3	102	4	US-09-821-976-11436	Sequence 11436, A
40	23	2.3	319	4	US-07-593-657-14	Sequence 14, Appli
41	23	2.3	373	4	US-09-621-976-18454	Sequence 18454, A
42	23	2.3	458	2	US-08-924-759-7	Sequence 7, Appli
43	23	2.3	458	3	US-09-348-335-7	Sequence 7, Appli
44	23	2.3	487	4	US-09-257-179-22	Sequence 22, Appli
45	23	2.3	521	3	US-09-488-744B-10	Sequence 10, Appli
c 46	23	2.3	545	3	US-09-328-111-506	Sequence 506, App
47	23	2.3	681	4	US-09-410-464-3	Sequence 3, Appli
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49	23	2.3	1112	4	US-09-173-300-48	Sequence 48, Appli
50	23	2.3	1213	1	US-08-276-151-6	Sequence 6, Appli
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56	23	2.3	1318	4	US-09-719-108-5	Sequence 5, Appli
57	23	2.3	1334	4	US-09-434-690-1	Sequence 1, Appli
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59	23	2.3	1364	2	US-08-872-302-3	Sequence 3, Appli
60	23	2.3	1581	2	US-08-845-998-1	Sequence 1, Appli
61	23	2.3	1581	3	US-09-206-537-1	Sequence 1, Appli
62	23	2.3	1581	3	US-09-430-854-1	Sequence 1, Appli
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64	23	2.3	2132	2	US-09-159-385-3	Sequence 3, Appli
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69	23	2.3	3268	4	US-09-566-921-91	Sequence 91, Appli
70	23	2.3	3708	3	US-08-556-419-10	Sequence 10, Appli
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c 74	22	2.2	24	4	US-09-721-154-1	Sequence 1, Appli
c 75	22	2.2	27	4	US-09-475-947A-153	Sequence 153, App
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78	22	2.2	36	1	US-08-113-646A-43	Sequence 43, Appli
79	22	2.2	37	1	US-08-113-646A-38	Sequence 38, Appli
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c 81	22	2.2	39	3	US-09-306-290-40	Sequence 40, Appli
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c 83	22	2.2	43	3	US-09-306-290-1	Sequence 1, Appli
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89	22	2.2	66	4	US-09-621-976-12102	Sequence 12102, A
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91	22	2.2	68	4	US-09-621-976-11912	Sequence 11912, A
92	22	2.2	68	4	US-09-621-976-12005	Sequence 12005, A
93	22	2.2	69	4	US-09-621-976-12006	Sequence 12006, A
94	22	2.2	70	4	US-09-621-976-13579	Sequence 13579, A
95	22	2.2	76	4	US-09-621-976-12446	Sequence 12446, A
96	22	2.2	83	1	US-08-120-827-92	Sequence 92, Appli
97	22	2.2	83	1	US-08-478-675-92	Sequence 92, Appli
98	22	2.2	110	4	US-09-621-976-12025	Sequence 12025, A
99	22	2.2	116	4	US-09-621-976-10586	Sequence 10586, A
100	22	2.2	118	4	US-09-621-976-17444	Sequence 17444, A

101	22	2.2	2.2	119	4	US-09-621-976-9434	Sequence 9434, Ap	c 174	22	2.2	608	3	US-09-385-982-183	Sequence 183, App
102	22	2.2	2.2	129	4	US-09-621-976-17454	Sequence 17454, A	c 175	22	2.2	609	1	US-08-530-797-9	Sequence 9, Appl
103	22	2.2	2.2	130	4	US-09-621-976-17455	Sequence 17455, A	c 176	22	2.2	609	2	US-08-787-335-9	Sequence 9, Appl
104	22	2.2	2.2	131	4	US-09-621-976-17453	Sequence 17453, A	c 177	22	2.2	611	3	US-09-385-982-376	Sequence 376, App
105	22	2.2	2.2	132	4	US-09-621-976-13468	Sequence 13468, A	c 178	22	2.2	611	4	US-09-376-113-4	Sequence 4, Appl
106	22	2.2	2.2	133	4	US-09-621-976-13468	Sequence 13468, A	c 179	22	2.2	624	3	US-09-385-982-509	Sequence 509, App
107	22	2.2	2.2	140	4	US-09-621-976-17449	Sequence 17449, A	c 180	22	2.2	631	4	US-09-376-113-6	Sequence 6, Appl
108	22	2.2	2.2	140	4	US-09-621-976-17457	Sequence 17457, A	c 181	22	2.2	632	3	US-09-385-982-507	Sequence 507, App
109	22	2.2	2.2	141	3	US-08-737-078A-1	Sequence 1, Appl	c 182	22	2.2	633	1	US-08-664-596B-21	Sequence 21, Appl
110	22	2.2	2.2	141	4	US-09-621-976-17446	Sequence 17446, A	c 183	22	2.2	634	4	US-09-669-751-2	Sequence 2, Appl
111	22	2.2	2.2	141	5	PCT-US94-04706-1	Sequence 1, Appl	c 184	22	2.2	724	4	US-09-724-864-23	Sequence 23, Appl
112	22	2.2	2.2	148	4	US-09-621-976-17447	Sequence 17447, A	c 185	22	2.2	732	4	US-09-437-054A-15	Sequence 15, Appl
113	22	2.2	2.2	148	4	US-09-621-976-17450	Sequence 17450, A	c 186	22	2.2	746	3	US-09-013-810-1	Sequence 1, Appl
114	22	2.2	2.2	153	4	US-09-621-976-17451	Sequence 17451, A	c 187	22	2.2	748	1	US-08-361-467B-3	Sequence 3, Appl
115	22	2.2	2.2	177	4	US-09-621-976-9899	Sequence 9899, Ap	c 188	22	2.2	748	1	US-08-484-332C-3	Sequence 3, Appl
116	22	2.2	2.2	180	2	US-08-250-346-4	Sequence 4, Appl	c 189	22	2.2	755	3	US-09-385-982-536	Sequence 536, App
117	22	2.2	2.2	181	4	US-09-621-976-18027	Sequence 18027, A	c 190	22	2.2	760	1	US-08-276-452A-49	Sequence 49, Appl
118	22	2.2	2.2	183	3	US-09-040-984-56	Sequence 56, Appl	c 191	22	2.2	760	2	US-08-798-744-49	Sequence 49, Appl
119	22	2.2	2.2	183	4	US-09-123-912-56	Sequence 56, Appl	c 192	22	2.2	760	4	US-09-205-258-232	Sequence 232, App
120	22	2.2	2.2	183	4	US-09-643-587-56	Sequence 56, Appl	c 193	22	2.2	760	4	US-09-668-282A-19	Sequence 19, Appl
121	22	2.2	2.2	183	4	US-09-480-884A-56	Sequence 56, Appl	c 194	22	2.2	773	3	US-09-248-335-39	Sequence 39, Appl
122	22	2.2	2.2	183	4	US-09-542-615A-56	Sequence 56, Appl	c 195	22	2.2	773	3	US-09-248-335-39	Sequence 2, Appl
123	22	2.2	2.2	183	4	US-09-606-421B-56	Sequence 56, Appl	c 196	22	2.2	813	4	US-09-370-838-29	Sequence 29, Appl
124	22	2.2	2.2	183	4	US-09-221-107-56	Sequence 56, Appl	c 197	22	2.2	815	4	US-09-369-247-15	Sequence 15, Appl
125	22	2.2	2.2	187	4	US-09-621-976-18028	Sequence 18028, A	c 198	22	2.2	819	4	US-09-328-475C-236	Sequence 236, App
126	22	2.2	2.2	207	4	US-09-621-976-10240	Sequence 10240, A	c 199	22	2.2	840	2	US-08-924-759-13	Sequence 13, Appl
127	22	2.2	2.2	236	4	US-09-621-976-10240	Sequence 10240, A	c 200	22	2.2	840	3	US-09-248-335-13	Sequence 13, Appl
128	22	2.2	2.2	241	4	US-09-621-976-17924	Sequence 17924, A	c 201	22	2.2	855	3	US-09-060-726A-1	Sequence 1, Appl
129	22	2.2	2.2	241	4	US-09-621-976-17936	Sequence 17936, A	c 202	22	2.2	856	3	US-09-060-726A-3	Sequence 3, Appl
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131	22	2.2	2.2	243	4	US-09-621-976-17939	Sequence 17939, A	c 204	22	2.2	867	4	US-09-262-537-13	Sequence 13, Appl
132	22	2.2	2.2	243	4	US-09-621-976-17940	Sequence 17940, A	c 205	22	2.2	870	5	PCT-US95-13658-3	Sequence 3, Appl
133	22	2.2	2.2	247	4	US-09-621-976-17938	Sequence 17938, A	c 206	22	2.2	882	3	US-09-068-140A-1	Sequence 1, Appl
134	22	2.2	2.2	248	4	US-09-621-976-17931	Sequence 17931, A	c 207	22	2.2	887	4	US-09-010-147B-3	Sequence 3, Appl
135	22	2.2	2.2	262	4	US-09-621-976-17925	Sequence 17925, A	c 208	22	2.2	900	3	PCT-US95-06406A-21	Sequence 21, Appl
136	22	2.2	2.2	270	4	US-09-621-976-17927	Sequence 17927, A	c 209	22	2.2	903	5	US-09-248-335-61	Sequence 61, Appl
137	22	2.2	2.2	277	4	US-09-621-976-16983	Sequence 16983, A	c 210	22	2.2	911	4	US-09-461-325-63	Sequence 63, Appl
138	22	2.2	2.2	289	1	US-08-341-568-3	Sequence 3, Appl	c 211	22	2.2	911	4	US-10-012-542-63	Sequence 63, Appl
139	22	2.2	2.2	313	1	US-08-911-020-3	Sequence 3, Appl	c 212	22	2.2	923	4	US-09-336-643A-15	Sequence 15, Appl
140	22	2.2	2.2	313	4	US-08-686-878A-28	Sequence 28, Appl	c 213	22	2.2	933	4	US-09-301-666A-1	Sequence 1, Appl
141	22	2.2	2.2	313	4	US-09-175-928-28	Sequence 28, Appl	c 214	22	2.2	933	4	US-09-301-666A-1	Sequence 1, Appl
142	22	2.2	2.2	315	4	US-09-621-976-15329	Sequence 15329, A	c 215	22	2.2	933	3	US-08-924-747-19	Sequence 19, Appl
143	22	2.2	2.2	333	4	US-09-328-111-797	Sequence 18236, A	c 216	22	2.2	935	3	US-08-247-373B-19	Sequence 19, Appl
144	22	2.2	2.2	337	4	US-09-621-976-18236	Sequence 48, Appl	c 217	22	2.2	935	3	US-09-296-715-19	Sequence 19, Appl
145	22	2.2	2.2	350	1	US-08-276-452A-48	Sequence 48, Appl	c 218	22	2.2	948	3	US-08-924-759-11	Sequence 11, Appl
146	22	2.2	2.2	350	2	US-08-798-744-48	Sequence 48, Appl	c 219	22	2.2	948	3	US-09-248-335-11	Sequence 11, Appl
147	22	2.2	2.2	358	1	US-08-686-878A-3	Sequence 3, Appl	c 220	22	2.2	970	4	US-09-833-381-1294	Sequence 1294, Ap
148	22	2.2	2.2	370	4	US-09-376-113-1	Sequence 1, Appl	c 221	22	2.2	984	4	US-09-230-665-7	Sequence 7, Appl
149	22	2.2	2.2	373	4	US-09-621-976-17213	Sequence 17213, A	c 222	22	2.2	993	4	US-09-464-535-25	Sequence 25, Appl
150	22	2.2	2.2	382	4	US-09-621-976-18855	Sequence 18855, A	c 223	22	2.2	1007	4	US-09-171-156A-61	Sequence 61, Appl
151	22	2.2	2.2	422	4	US-09-177-304-1	Sequence 1, Appl	c 224	22	2.2	1007	4	US-09-171-156A-63	Sequence 63, Appl
152	22	2.2	2.2	444	3	US-09-328-111-436	Sequence 436, App	c 225	22	2.2	1007	4	US-09-004-730A-61	Sequence 61, Appl
153	22	2.2	2.2	469	3	US-09-688-988-44	Sequence 44, Appl	c 226	22	2.2	1007	4	US-09-004-730A-63	Sequence 63, Appl
154	22	2.2	2.2	488	4	US-09-482-273-54	Sequence 54, Appl	c 227	22	2.2	1007	4	US-09-004-730A-63	Sequence 63, Appl
155	22	2.2	2.2	490	2	US-08-630-822A-92	Sequence 92, Appl	c 228	22	2.2	1007	4	US-08-981-799A-61	Sequence 61, Appl
156	22	2.2	2.2	490	2	US-08-085-089-52	Sequence 92, Appl	c 229	22	2.2	1016	4	US-08-981-799A-63	Sequence 63, Appl
157	22	2.2	2.2	490	4	US-09-171-156A-41	Sequence 41, Appl	c 230	22	2.2	1024	4	US-09-716-129-42	Sequence 42, Appl
158	22	2.2	2.2	490	4	US-09-004-730A-41	Sequence 41, Appl	c 231	22	2.2	1024	4	US-09-425-578-5	Sequence 5, Appl
159	22	2.2	2.2	490	4	US-08-981-799A-41	Sequence 41, Appl	c 232	22	2.2	1024	4	US-09-615-192A-135	Sequence 135, App
160	22	2.2	2.2	498	4	US-09-621-976-14179	Sequence 14179, A	c 233	22	2.2	1024	4	US-09-328-475C-20	Sequence 20, Appl
161	22	2.2	2.2	499	4	US-09-621-976-8143	Sequence 8143, Ap	c 234	22	2.2	1024	4	US-09-328-475C-63	Sequence 63, Appl
162	22	2.2	2.2	519	4	US-09-205-258-180	Sequence 180, App	c 235	22	2.2	1024	4	US-09-169-789-135	Sequence 135, App
163	22	2.2	2.2	546	4	US-08-280-116-48	Sequence 48, Appl	c 236	22	2.2	1031	4	US-08-833-381-1634	Sequence 1634, Ap
164	22	2.2	2.2	547	3	US-09-188-930-14	Sequence 14, Appl	c 237	22	2.2	1033	4	US-09-610-185C-3	Sequence 3, Appl
165	22	2.2	2.2	547	4	US-09-312-283C-14	Sequence 14, Appl	c 238	22	2.2	1033	4	US-09-533-029-87	Sequence 87, Appl
166	22	2.2	2.2	549	3	US-09-091-590A-13	Sequence 13, Appl	c 239	22	2.2	1038	2	US-08-975-316-72	Sequence 72, Appl
167	22	2.2	2.2	550	3	US-08-632-511A-7	Sequence 7, Appl	c 240	22	2.2	1038	4	US-09-615-192A-72	Sequence 72, Appl
168	22	2.2	2.2	550	4	US-09-488-200-7	Sequence 7, Appl	c 241	22	2.2	1038	4	US-09-169-789-72	Sequence 72, Appl
169	22	2.2	2.2	563	4	US-09-621-976-19183	Sequence 19183, A	c 242	22	2.2	1058	4	US-09-452-239-11	Sequence 11, Appl
170	22	2.2	2.2	570	1	US-07-885-870A-10	Sequence 10, Appl	c 243	22	2.2	1066	4	US-08-634-912-43	Sequence 43, Appl
171	22	2.2	2.2	570	1	US-08-298-687A-10	Sequence 10, Appl	c 244	22	2.2	1089	4	US-09-796-766-13	Sequence 13, Appl
172	22	2.2	2.2	570	1	US-08-298-829-10	Sequence 10, Appl	c 245	22	2.2	1096	2	US-08-607-412-3	Sequence 3, Appl
173	22	2.2	2.2	585	4	US-09-257-179-14	Sequence 14, Appl	c 246	22	2.2	1108	4	US-09-800-729-42	Sequence 42, Appl

247	22	2.2	1123	4	US-09-614-912-159	Sequence 159, Appl	320	22	2.2	1523	4	US-09-022-765-21	Sequence 21, Appl
248	22	2.2	1132	3	US-08-894-731-3	Sequence 3, Appli	321	22	2.2	1523	4	US-09-551-974A-21	Sequence 21, Appl
249	22	2.2	1137	1	US-08-706-214-2	Sequence 2, Appli	322	22	2.2	1523	4	US-09-565-501A-21	Sequence 21, Appl
250	22	2.2	1141	4	US-09-800-729-78	Sequence 78, Appl	323	22	2.2	1523	4	US-09-639-206A-21	Sequence 21, Appl
251	22	2.2	1160	3	US-08-995-159-1	Sequence 1, Appli	324	22	2.2	1523	4	US-09-874-923-21	Sequence 33, Appl
252	22	2.2	1160	4	US-09-545-605-1	Sequence 1, Appli	325	22	2.2	1526	4	US-09-482-273-33	Sequence 17, Appl
253	22	2.2	1164	2	US-08-794-796-1	Sequence 1, Appli	326	22	2.2	1526	4	US-09-364-230-17	Sequence 17, Appl
254	22	2.2	1170	4	US-09-487-792-1	Sequence 1, Appli	327	22	2.2	1526	4	US-09-614-912-1	Sequence 1, Appli
255	22	2.2	1170	4	US-09-908-594-1	Sequence 1, Appli	328	22	2.2	1555	4	US-09-533-029-7	Sequence 7, Appli
256	22	2.2	1190	3	US-09-475-316A-61	Sequence 61, Appl	329	22	2.2	1557	4	US-08-455-550-7	Sequence 7, Appli
257	22	2.2	1190	4	US-09-390-207-1	Sequence 1, Appli	330	22	2.2	1558	1	US-08-821-994-59	Sequence 59, Appl
258	22	2.2	1190	4	US-09-704-640-61	Sequence 61, Appl	331	22	2.2	1577	3	US-09-183-861-54	Sequence 54, Appl
259	22	2.2	1226	4	US-09-668-097A-31	Sequence 31, Appl	332	22	2.2	1585	4	US-09-022-765-54	Sequence 54, Appl
260	22	2.2	1226	1	US-08-181-271A-39	Sequence 39, Appl	333	22	2.2	1585	4	US-09-551-974A-54	Sequence 54, Appl
261	22	2.2	1250	1	US-08-443-315-39	Sequence 39, Appl	334	22	2.2	1585	4	US-09-565-501A-54	Sequence 54, Appl
262	22	2.2	1250	1	US-08-444-803-39	Sequence 39, Appl	335	22	2.2	1585	4	US-09-639-206A-54	Sequence 54, Appl
263	22	2.2	1250	1	US-08-443-803-39	Sequence 39, Appl	336	22	2.2	1585	4	US-09-874-923-54	Sequence 54, Appl
264	22	2.2	1250	1	US-08-456-265A-39	Sequence 39, Appl	337	22	2.2	1600	3	US-07-861-458C-37	Patent No. 5196333
265	22	2.2	1250	1	US-08-455-416-39	Sequence 39, Appl	338	22	2.2	1607	6	5196333-3	Sequence 3, Appli
266	22	2.2	1250	1	US-08-455-244-39	Sequence 39, Appl	339	22	2.2	1613	4	US-08-965-048-3	Sequence 3, Appli
267	22	2.2	1250	1	US-08-454-876-39	Sequence 39, Appl	340	22	2.2	1638	2	US-08-541-759B-1	Sequence 1, Appli
268	22	2.2	1250	2	US-08-457-364-39	Sequence 39, Appl	341	22	2.2	1641	1	US-08-300-903A-8	Sequence 8, Appli
269	22	2.2	1250	2	US-08-458-262-39	Sequence 39, Appl	342	22	2.2	1641	4	US-08-988-197-8	Sequence 8, Appli
270	22	2.2	1250	2	US-08-458-240-39	Sequence 39, Appl	343	22	2.2	1655	4	US-10-132-920B-1	Sequence 1, Appli
271	22	2.2	1250	2	US-08-455-736-39	Sequence 39, Appl	344	22	2.2	1661	3	US-08-821-994-82	Sequence 82, Appl
272	22	2.2	1250	2	US-08-971-217-39	Sequence 39, Appl	345	22	2.2	1663	4	US-09-614-912-127	Sequence 127, App
273	22	2.2	1250	3	US-09-350-600-39	Sequence 39, Appl	346	22	2.2	1672	2	US-08-684-101-1	Sequence 1, Appli
274	22	2.2	1250	4	US-09-906-234-39	Sequence 39, Appl	347	22	2.2	1677	3	US-09-205-814-1	Sequence 1, Appli
275	22	2.2	1272	3	US-09-053-702-1	Sequence 1, Appli	348	22	2.2	1703	1	US-07-868-353A-11	Sequence 11, Appl
276	22	2.2	1273	1	US-08-507-431-1	Sequence 1, Appli	349	22	2.2	1703	1	US-08-407-804-20	Sequence 20, Appl
277	22	2.2	1273	1	US-08-902-655A-1	Sequence 1, Appli	350	22	2.2	1703	3	US-09-124-807-20	Sequence 20, Appl
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279	22	2.2	1273	3	US-09-219-277-1	Sequence 1, Appli	352	22	2.2	1736	3	US-09-182-816-22	Sequence 22, Appl
280	22	2.2	1273	3	US-09-599-661-1	Sequence 1, Appli	353	22	2.2	1736	3	US-09-182-816-24	Sequence 24, Appl
281	22	2.2	1280	4	US-09-220-132-155	Sequence 155, App	354	22	2.2	1736	3	US-09-471-528-22	Sequence 22, Appl
282	22	2.2	1301	4	US-09-424-978B-10	Sequence 10, Appl	355	22	2.2	1736	3	US-09-471-528-24	Sequence 24, Appl
283	22	2.2	1327	4	US-09-843-287-1	Sequence 1, Appli	356	22	2.2	1736	3	US-09-634-530-24	Sequence 24, Appl
284	22	2.2	1332	4	US-09-412-600B-1	Sequence 1, Appli	357	22	2.2	1736	3	US-08-362-512A-3	Sequence 3, Appli
285	22	2.2	1337	4	US-09-220-132-131	Sequence 131, App	358	22	2.2	1740	1	US-08-964-939-3	Sequence 3, Appli
286	22	2.2	1361	4	US-09-489-847-64	Sequence 64, Appl	359	22	2.2	1740	4	US-09-149-476-68	Sequence 68, Appl
287	22	2.2	1366	4	US-09-149-476-49	Sequence 49, Appl	360	22	2.2	1751	4	US-09-667-135-3	Sequence 3, Appli
288	22	2.2	1370	4	US-09-026-408-12	Sequence 12, Appl	361	22	2.2	1759	4	US-09-033-055A-3	Sequence 3, Appli
289	22	2.2	1370	4	US-09-903-684-12	Sequence 12, Appl	362	22	2.2	1761	3	US-09-461-325-35	Sequence 35, Appl
290	22	2.2	1371	4	US-09-026-408-1	Sequence 1, Appli	363	22	2.2	1787	4	US-10-012-542-35	Sequence 35, Appl
291	22	2.2	1371	4	US-09-902-684-1	Sequence 1, Appli	364	22	2.2	1787	4	US-09-433-248A-5	Sequence 5, Appli
292	22	2.2	1374	3	US-08-672-850-9	Sequence 9, Appli	365	22	2.2	1831	4	US-08-795-430-10	Sequence 10, Appl
293	22	2.2	1374	4	US-09-565-177A-9	Sequence 9, Appli	366	22	2.2	1836	4	US-09-355-700-10	Sequence 10, Appl
294	22	2.2	1375	4	US-09-489-847-120	Sequence 120, App	367	22	2.2	1836	4	US-08-601-132-40	Sequence 40, Appl
295	22	2.2	1376	4	US-09-489-847-66	Sequence 66, Appl	368	22	2.2	1836	4	US-08-571-573B-40	Sequence 40, Appl
296	22	2.2	1377	4	US-09-866-028-41	Sequence 41, Appl	369	22	2.2	1836	4	US-08-750-134A-4	Sequence 4, Appli
297	22	2.2	1402	3	US-08-258-287B-56	Sequence 56, Appl	370	22	2.2	1837	2	US-09-363-745-4	Sequence 4, Appli
298	22	2.2	1402	3	US-08-368-704C-54	Sequence 54, Appl	371	22	2.2	1837	3	FCT-US95-00362-1	Sequence 1, Appli
299	22	2.2	1402	4	US-09-291-289-1	Sequence 1, Appli	372	22	2.2	1841	5	US-09-220-132-120	Sequence 120, App
300	22	2.2	1421	4	US-09-435-019-23	Sequence 23, Appl	373	22	2.2	1853	4	US-08-706-214-1	Sequence 1, Appli
301	22	2.2	1421	4	US-09-435-019-24	Sequence 24, Appl	374	22	2.2	1856	1	US-08-909-965C-11	Sequence 11, Appl
302	22	2.2	1424	4	US-09-326-186B-226	Sequence 226, App	375	22	2.2	1858	2	US-09-205-258-66	Sequence 66, Appl
303	22	2.2	1428	5	FCT-US94-09642-1	Sequence 1, Appli	376	22	2.2	1856	3	US-08-461-474-9	Sequence 9, Appli
304	22	2.2	1454	4	US-09-614-912-63	Sequence 63, Appl	377	22	2.2	1875	3	US-08-878-474-4	Sequence 4, Appli
305	22	2.2	1458	4	US-09-500-569-15	Sequence 15, Appl	378	22	2.2	1875	3	US-09-465-558-39	Sequence 39, Appl
306	22	2.2	1458	4	US-09-971-823B-15	Sequence 15, Appl	379	22	2.2	1878	4	US-09-517-467B-11	Sequence 11, Appl
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309	22	2.2	1473	1	US-08-232-249-3	Sequence 3, Appli	382	22	2.2	1917	2	US-09-325-430B-1	Sequence 1, Appli
310	22	2.2	1473	2	US-08-833-642A-3	Sequence 3, Appli	383	22	2.2	1917	3	US-08-614-912-173	Sequence 173, App
311	22	2.2	1473	2	US-08-389-423-3	Sequence 3, Appli	384	22	2.2	1917	2	US-08-353-436A-1	Sequence 1, Appli
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315	22	2.2	1490	4	US-09-496-692-3	Sequence 3, Appli	388	22	2.2	1931	4	US-09-470-271-2	Sequence 2, Appli
316	22	2.2	1490	4	US-10-000-273-3	Sequence 3, Appli	389	22	2.2	1931	4	US-09-307-359B-1	Sequence 1, Appli
317	22	2.2	1494	2	US-08-605-106-1	Sequence 1, Appli	390	22	2.2	1931	4	US-09-340-620A-1	Sequence 1, Appli
318	22	2.2	1502	4	US-09-369-247-33	Sequence 33, Appl	391	22	2.2	1931	4	US-09-865-364-1	Sequence 1, Appli
319	22	2.2	1523	4	US-09-183-861-21	Sequence 21, Appl	392	22	2.2	1931	4		

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394	22	2.2	1932	4	US-09-482-273-39	Sequence 39, Appli	467	22	2.2	2861	3	US-09-175-581-12	Sequence 12, Appli
395	22	2.2	1933	4	US-08-776-844-1	Sequence 1, Appli	468	22	2.2	2880	4	US-09-235-451-1	Sequence 1, Appli
396	22	2.2	1934	4	US-09-909-325-1	Sequence 1, Appli	469	22	2.2	2890	4	US-09-205-258-150	Sequence 150, Appli
397	22	2.2	1934	4	US-09-909-326-1	Sequence 1, Appli	470	22	2.2	2908	4	US-09-930-181-1	Sequence 1, Appli
398	22	2.2	1944	4	US-09-149-476-144	Sequence 144, App	C 471	22	2.2	2914	1	US-08-454-097-11	Sequence 11, Appli
399	22	2.2	1946	4	US-09-833-361-896	Sequence 896, App	C 472	22	2.2	2914	3	US-08-185-359-11	Sequence 11, Appli
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402	22	2.2	1972	4	US-09-370-098-1	Sequence 1, Appli	475	22	2.2	3250	1	US-07-718-575-9	Sequence 9, Appli
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C 404	22	2.2	2007	3	US-08-747-221B-36	Sequence 36, Appli	477	22	2.2	3250	4	US-08-486-269A-9	Sequence 9, Appli
C 405	22	2.2	2007	3	US-08-747-221B-38	Sequence 38, Appli	478	22	2.2	3262	2	US-09-561-989-9	Sequence 9, Appli
C 406	22	2.2	2007	3	US-09-005-051-36	Sequence 36, Appli	479	22	2.2	3319	2	US-08-960-022-19	Sequence 19, Appli
C 407	22	2.2	2007	3	US-09-005-051-38	Sequence 38, Appli	480	22	2.2	3364	2	US-08-735-609-9	Sequence 9, Appli
C 408	22	2.2	2007	4	US-09-403-942F-36	Sequence 36, Appli	481	22	2.2	3364	2	US-08-735-609-9	Sequence 9, Appli
C 409	22	2.2	2007	4	US-09-403-942F-38	Sequence 38, Appli	482	22	2.2	3364	3	US-09-315-372-9	Sequence 9, Appli
C 410	22	2.2	2013	4	US-10-132-920B-26	Sequence 26, Appli	483	22	2.2	3364	3	US-09-244-752-9	Sequence 9, Appli
C 411	22	2.2	2044	4	US-09-889-463A-27	Sequence 27, Appli	484	22	2.2	3364	3	US-09-245-497-9	Sequence 9, Appli
C 412	22	2.2	2046	4	US-09-057-996-5	Sequence 5, Appli	485	22	2.2	3364	4	US-09-562-919-9	Sequence 9, Appli
C 413	22	2.2	2066	4	US-09-205-258-105	Sequence 105, App	486	22	2.2	3383	3	US-08-861-105-13	Sequence 13, Appli
C 414	22	2.2	2074	4	US-09-220-132-7	Sequence 132, App	487	22	2.2	3383	3	US-08-575-967A-1	Sequence 1, Appli
C 415	22	2.2	2074	4	US-09-220-132-138	Sequence 138, App	488	22	2.2	3383	4	US-09-023-655-951	Sequence 951, App
C 416	22	2.2	2083	3	US-08-574-959A-1	Sequence 1, Appli	489	22	2.2	3411	4	US-08-890-865A-3	Sequence 3, Appli
C 417	22	2.2	2083	3	US-09-357-014-1	Sequence 1, Appli	490	22	2.2	3434	4	US-09-439-313-476	Sequence 476, App
C 418	22	2.2	2092	4	US-09-219-983A-27	Sequence 27, Appli	491	22	2.2	3434	4	US-09-636-215-476	Sequence 476, App
C 419	22	2.2	2134	2	US-08-483-151-3	Sequence 3, Appli	492	22	2.2	3434	4	US-09-685-165A-476	Sequence 476, App
C 420	22	2.2	2134	5	PCT-US96-06427-3	Sequence 3, Appli	C 493	22	2.2	3480	4	US-09-331-359-1	Sequence 1, Appli
C 421	22	2.2	2143	4	US-08-656-177A-1	Sequence 1, Appli	494	22	2.2	3516	2	US-08-943-087-1	Sequence 1, Appli
C 422	22	2.2	2143	3	US-09-256-797-1	Sequence 1, Appli	495	22	2.2	3516	4	US-09-746-359A-10	Sequence 10, Appli
C 423	22	2.2	2160	4	US-09-716-129-12	Sequence 12, Appli	496	22	2.2	3516	4	US-09-861-779-1	Sequence 1, Appli
C 424	22	2.2	2166	4	US-09-175-928-1	Sequence 1, Appli	497	22	2.2	3606	4	US-10-164-595-37	Sequence 37, Appli
C 425	22	2.2	2172	2	US-08-417-174-26	Sequence 26, Appli	498	22	2.2	3636	3	US-09-074-579-2	Sequence 2, Appli
C 426	22	2.2	2172	2	US-08-231-565A-26	Sequence 26, Appli	499	22	2.2	3636	4	US-09-388-774-2	Sequence 2, Appli
C 427	22	2.2	2172	2	US-09-007-961-26	Sequence 26, Appli	500	22	2.2	3667	4	US-09-511-625B-1	Sequence 1, Appli
C 428	22	2.2	2172	3	US-08-267-439-26	Sequence 26, Appli	501	22	2.2	3825	3	US-09-208-742-3	Sequence 3, Appli
C 429	22	2.2	2172	4	US-09-073-138-26	Sequence 26, Appli	502	22	2.2	3901	1	US-08-188-582-31	Sequence 31, Appli
C 430	22	2.2	2190	4	US-09-015-188-1	Sequence 1, Appli	503	22	2.2	3901	1	US-08-646-715-31	Sequence 31, Appli
C 431	22	2.2	2210	4	US-09-786-261-1	Sequence 1, Appli	504	22	2.2	4182	4	US-09-667-432-2	Sequence 2, Appli
C 432	22	2.2	2218	4	US-09-205-258-103	Sequence 103, App	505	22	2.2	4203	4	US-09-667-432-1	Sequence 1, Appli
C 433	22	2.2	2239	4	US-09-581-831-1	Sequence 1, Appli	506	22	2.2	4235	4	US-09-342-681C-18	Sequence 18, Appli
C 434	22	2.2	2303	4	US-09-922-146-3	Sequence 3, Appli	507	22	2.2	4673	1	US-07-638-431-1	Sequence 1, Appli
C 435	22	2.2	2329	4	US-09-800-729-11	Sequence 11, Appli	508	22	2.2	4673	5	PCT-US92-00018-1	Sequence 1, Appli
C 436	22	2.2	2353	4	US-09-369-247-12	Sequence 12, Appli	509	22	2.2	4745	4	US-09-713-273A-19	Sequence 19, Appli
C 437	22	2.2	2355	4	US-09-800-729-27	Sequence 27, Appli	510	22	2.2	4803	3	US-09-197-636-1	Sequence 1, Appli
C 438	22	2.2	2369	4	US-09-057-996-13	Sequence 13, Appli	511	22	2.2	4803	3	US-09-197-636-3	Sequence 3, Appli
C 439	22	2.2	2370	4	US-09-031-295-1	Sequence 1, Appli	C 512	22	2.2	5108	1	US-07-642-002-1	Sequence 1, Appli
C 440	22	2.2	2389	4	US-09-799-875-7	Sequence 7, Appli	513	22	2.2	5152	4	US-10-204-708-74	Sequence 74, Appli
C 441	22	2.2	2405	2	US-08-687-702-2	Sequence 2, Appli	514	22	2.2	5170	4	US-09-677-046A-5	Sequence 5, Appli
C 442	22	2.2	2413	2	US-08-651-579-1	Sequence 1, Appli	515	22	2.2	5173	1	US-08-242-677-1	Sequence 1, Appli
C 443	22	2.2	2434	4	US-09-489-847-67	Sequence 67, Appli	C 516	22	2.2	5314	4	US-10-204-708-16	Sequence 16, Appli
C 444	22	2.2	2483	4	US-09-205-258-68	Sequence 68, Appli	517	22	2.2	5360	4	US-10-204-708-66	Sequence 66, Appli
C 445	22	2.2	2497	4	US-08-396-149-1	Sequence 1, Appli	518	22	2.2	5490	4	US-09-607-510-1	Sequence 1, Appli
C 446	22	2.2	2500	4	US-09-962-665-9	Sequence 9, Appli	519	22	2.2	5535	4	US-10-204-708-17	Sequence 17, Appli
C 447	22	2.2	2500	4	US-09-023-655-1370	Sequence 1370, Ap	C 520	22	2.2	5852	1	US-07-867-106-2	Sequence 2, Appli
C 448	22	2.2	2500	4	US-09-963-333-9	Sequence 9, Appli	C 521	22	2.2	6070	4	US-10-204-708-10	Sequence 10, Appli
C 449	22	2.2	2525	4	US-08-294-312B-1	Sequence 1, Appli	522	22	2.2	6152	3	US-08-973-462-1	Sequence 1, Appli
C 450	22	2.2	2525	4	US-08-468-024B-1	Sequence 1, Appli	523	22	2.2	6326	4	US-10-204-708-58	Sequence 58, Appli
C 451	22	2.2	2525	4	US-08-187-757D-1	Sequence 1, Appli	C 524	22	2.2	8093	4	US-10-204-708-31	Sequence 31, Appli
C 452	22	2.2	2525	4	US-08-465-679-1	Sequence 1, Appli	C 525	22	2.2	8093	4	US-10-204-708-32	Sequence 32, Appli
C 453	22	2.2	2525	4	US-08-210-143C-1	Sequence 1, Appli	526	22	2.2	8220	2	US-08-568-459A-11	Sequence 11, Appli
C 454	22	2.2	2552	4	US-09-833-381-1635	Sequence 1635, Ap	527	22	2.2	8220	2	US-08-487-826B-11	Sequence 11, Appli
C 455	22	2.2	2571	4	US-03-620-312D-302	Sequence 302, App	528	22	2.2	8220	4	US-09-210-288-11	Sequence 11, Appli
C 456	22	2.2	2618	4	US-09-857-556A-25	Sequence 25, Appli	529	22	2.2	8239	4	US-09-029-047C-1	Sequence 1, Appli
C 457	22	2.2	2643	4	US-09-016-434-1398	Sequence 1398, Ap	C 530	22	2.2	8607	4	US-10-204-708-71	Sequence 71, Appli
C 458	22	2.2	2678	1	US-08-724-194-2	Sequence 2, Appli	C 531	22	2.2	8607	4	US-10-204-708-72	Sequence 72, Appli
C 459	22	2.2	2706	4	US-09-463-238-2	Sequence 2, Appli	532	22	2.2	10136	1	US-08-353-700-2	Sequence 2, Appli
C 460	22	2.2	2760	1	US-08-101-593-1	Sequence 1, Appli	533	22	2.2	10136	5	PCT-US95-16216-2	Sequence 2, Appli
C 461	22	2.2	2760	1	US-08-101-593-3	Sequence 3, Appli	534	22	2.2	10467	4	US-10-204-708-1	Sequence 1, Appli
C 462	22	2.2	2805	4	US-08-463-238-11	Sequence 11, Appli	C 535	22	2.2	10640	4	US-09-417-485D-5	Sequence 5, Appli
C 463	22	2.2	2823	1	US-08-398-008A-1	Sequence 1, Appli	536	22	2.2	10640	4	US-10-204-708-85	Sequence 85, Appli
C 464	22	2.2	2823	1	US-08-893-333-1	Sequence 1, Appli	537	22	2.2	17656	4	US-09-433-579-3	Sequence 3, Appli
C 465	22	2.2	2844	4	US-09-519-232-65	Sequence 65, Appli	538	22	2.2	19124	2	US-08-487-826B-13	Sequence 13, Appli

C 539	22	2.2	19233	4	US-10-204-708-46	Sequence 46, Appl	612	21	2.1	105	3	US-08-746-111-37	Sequence 37, Appl
C 540	22	2.2	19557	5	PT-US92-06300-1	Sequence 1, Appl	C 613	21	2.1	105	4	US-09-284-627-23	Sequence 23, Appl
C 541	22	2.2	20284	4	US-09-526-193A-21	Sequence 21, Appl	614	21	2.1	106	4	US-09-621-976-14212	Sequence 14212, A
C 542	22	2.2	168575	4	US-09-426-290-1	Sequence 1, Appl	615	21	2.1	107	4	US-09-621-976-16687	Sequence 16687, A
C 543	21	2.1	24	4	US-09-168-249B-6	Sequence 6, Appl	616	21	2.1	108	4	US-09-621-976-16693	Sequence 16693, A
C 544	21	2.1	26	1	US-08-621-914A-1	Sequence 1, Appl	617	21	2.1	109	1	US-08-120-827-82	Sequence 82, Appl
C 545	21	2.1	26	4	US-09-522-217-38	Sequence 38, Appl	618	21	2.1	109	1	US-08-478-675-82	Sequence 82, Appl
C 546	21	2.1	26	4	US-09-527-345-7	Sequence 7, Appl	619	21	2.1	111	4	US-09-621-976-9656	Sequence 9656, Ap
C 547	21	2.1	26	4	US-09-923-246-38	Sequence 38, Appl	620	21	2.1	111	4	US-09-621-976-16594	Sequence 16594, A
C 548	21	2.1	26	4	US-10-295-723-38	Sequence 38, Appl	621	21	2.1	112	4	US-09-621-976-13965	Sequence 13965, A
C 549	21	2.1	32	4	US-10-003-988A-4	Sequence 4, Appl	622	21	2.1	112	4	US-09-621-976-16685	Sequence 16685, A
C 550	21	2.1	34	1	US-08-113-646A-36	Sequence 36, Appl	C 623	21	2.1	113	4	US-09-367-927A-1	Sequence 1, Appl
C 551	21	2.1	39	4	US-09-619-103-4	Sequence 4, Appl	624	21	2.1	114	1	US-08-120-827-99	Sequence 99, Appl
C 552	21	2.1	40	1	US-08-510-032A-2	Sequence 2, Appl	625	21	2.1	114	1	US-08-478-675-99	Sequence 99, Appl
C 553	21	2.1	40	3	US-08-688-514-2	Sequence 2, Appl	626	21	2.1	114	4	US-09-621-976-9972	Sequence 9972, Ap
C 554	21	2.1	40	3	US-09-306-290-7	Sequence 7, Appl	C 627	21	2.1	114	4	US-09-621-976-14886	Sequence 14886, A
C 555	21	2.1	40	3	US-09-306-290-8	Sequence 8, Appl	628	21	2.1	115	4	US-09-453-190B-9	Sequence 9, Appl
C 556	21	2.1	40	3	US-09-306-290-11	Sequence 11, Appl	629	21	2.1	115	4	US-09-621-976-9586	Sequence 9586, Ap
C 557	21	2.1	40	3	US-09-306-290-14	Sequence 14, Appl	630	21	2.1	115	4	US-09-621-976-14003	Sequence 14003, A
C 558	21	2.1	40	3	US-09-306-290-16	Sequence 16, Appl	631	21	2.1	118	4	US-09-621-976-16690	Sequence 16690, A
C 559	21	2.1	40	3	US-09-306-290-33	Sequence 33, Appl	632	21	2.1	119	4	US-09-621-976-10024	Sequence 10024, A
C 560	21	2.1	40	3	US-09-306-290-34	Sequence 34, Appl	633	21	2.1	119	4	US-09-621-976-10154	Sequence 10154, A
C 561	21	2.1	40	3	US-09-306-290-35	Sequence 35, Appl	634	21	2.1	119	4	US-09-621-976-10154	Sequence 10154, A
C 562	21	2.1	40	3	US-09-306-290-36	Sequence 36, Appl	635	21	2.1	120	1	US-08-153-051B-28	Sequence 28, Appl
C 563	21	2.1	40	4	US-09-506-729-5	Sequence 5, Appl	636	21	2.1	120	1	US-08-060-952C-44	Sequence 44, Appl
C 564	21	2.1	42	4	US-09-536-936-8	Sequence 8, Appl	637	21	2.1	120	2	US-08-151-477A-28	Sequence 28, Appl
C 565	21	2.1	42	4	US-09-536-936-9	Sequence 9, Appl	638	21	2.1	120	3	US-08-819-867-58	Sequence 58, Appl
C 566	21	2.1	43	2	US-08-686-599A-14	Sequence 14, Appl	639	21	2.1	120	4	US-08-464-011B-44	Sequence 44, Appl
C 567	21	2.1	45	1	US-08-522-623-6	Sequence 6, Appl	640	21	2.1	120	4	US-09-378-535-58	Sequence 58, Appl
C 568	21	2.1	45	1	US-08-522-623-11	Sequence 11, Appl	641	21	2.1	120	4	US-09-621-976-10051	Sequence 10051, A
C 569	21	2.1	45	1	US-08-792-019B-15	Sequence 15, Appl	642	21	2.1	120	4	US-09-621-976-16689	Sequence 16689, A
C 570	21	2.1	45	3	US-08-988-819-15	Sequence 15, Appl	643	21	2.1	127	4	US-09-621-976-16696	Sequence 16696, A
C 571	21	2.1	45	3	US-08-988-819-15	Sequence 15, Appl	644	21	2.1	130	4	US-09-621-976-12892	Sequence 12892, A
C 572	21	2.1	45	5	PT-US93-03256-6	Sequence 6, Appl	645	21	2.1	135	2	US-08-799-464A-35	Sequence 35, Appl
C 573	21	2.1	45	5	PT-US93-03256-11	Sequence 11, Appl	646	21	2.1	138	4	US-09-621-976-9595	Sequence 9595, Ap
C 574	21	2.1	46	2	US-08-663-688A-4	Sequence 4, Appl	647	21	2.1	140	1	US-08-628-417-5	Sequence 5, Appl
C 575	21	2.1	47	3	US-09-338-907-198	Sequence 198, App	648	21	2.1	140	4	US-09-621-976-10526	Sequence 10526, A
C 576	21	2.1	47	3	US-09-338-907-275	Sequence 275, App	649	21	2.1	141	4	US-09-621-976-8705	Sequence 8705, Ap
C 577	21	2.1	47	4	US-09-218-207-198	Sequence 198, App	650	21	2.1	142	4	US-09-621-976-10561	Sequence 10561, A
C 578	21	2.1	47	4	US-09-218-207-275	Sequence 275, App	651	21	2.1	144	1	US-08-702-344-26	Sequence 26, Appl
C 579	21	2.1	48	2	US-08-563-368B-14	Sequence 14, Appl	652	21	2.1	144	4	US-09-702-705-776	Sequence 776, App
C 580	21	2.1	48	2	US-09-101-751A-14	Sequence 14, Appl	653	21	2.1	144	4	US-09-736-457-776	Sequence 776, App
C 581	21	2.1	48	4	US-09-738-274-35	Sequence 35, Appl	654	21	2.1	144	4	US-09-614-124B-776	Sequence 776, App
C 582	21	2.1	50	2	US-08-663-823B-72	Sequence 72, Appl	655	21	2.1	144	4	US-09-621-976-9868	Sequence 9868, Ap
C 583	21	2.1	51	4	US-09-453-190B-3	Sequence 3, Appl	656	21	2.1	144	4	US-09-671-325-776	Sequence 776, App
C 584	21	2.1	54	2	US-08-771-624B-24	Sequence 24, Appl	657	21	2.1	144	4	US-09-589-184-776	Sequence 776, App
C 585	21	2.1	54	4	US-09-611-627-2	Sequence 2, Appl	658	21	2.1	145	4	US-09-621-976-16688	Sequence 16688, A
C 586	21	2.1	54	4	US-09-611-627-45	Sequence 45, Appl	659	21	2.1	145	4	US-09-621-976-16691	Sequence 16691, A
C 587	21	2.1	55	4	US-09-944-036-32	Sequence 32, Appl	660	21	2.1	146	4	US-09-621-976-16686	Sequence 16686, A
C 588	21	2.1	56	3	US-09-425-383-5	Sequence 5, Appl	661	21	2.1	146	4	US-09-621-976-16695	Sequence 16695, A
C 589	21	2.1	56	4	US-09-944-036-30	Sequence 30, Appl	662	21	2.1	146	4	US-09-621-976-16695	Sequence 16695, A
C 590	21	2.1	56	4	US-09-611-627-4	Sequence 4, Appl	663	21	2.1	153	3	US-09-244-794A-3	Sequence 3, Appl
C 591	21	2.1	57	3	US-09-620-958A-7	Sequence 7, Appl	664	21	2.1	153	3	US-09-247-190-3	Sequence 3, Appl
C 592	21	2.1	57	4	US-09-944-036-31	Sequence 31, Appl	665	21	2.1	153	4	US-09-238-710-3	Sequence 3, Appl
C 593	21	2.1	57	4	US-09-611-627-6	Sequence 6, Appl	666	21	2.1	154	4	US-09-621-976-10847	Sequence 10847, A
C 594	21	2.1	57	4	US-09-621-976-11414	Sequence 11414, A	667	21	2.1	154	4	US-09-244-794A-17	Sequence 17, Appl
C 595	21	2.1	59	4	US-08-227-476-6	Sequence 6, Appl	668	21	2.1	159	3	US-09-247-190-17	Sequence 17, Appl
C 596	21	2.1	59	4	US-09-470-661A-26	Sequence 26, Appl	669	21	2.1	159	4	US-09-238-710-17	Sequence 17, Appl
C 597	21	2.1	59	4	US-09-621-976-14712	Sequence 14712, A	670	21	2.1	159	4	US-09-621-976-15312	Sequence 15312, A
C 598	21	2.1	60	4	US-09-621-976-14712	Sequence 14, Appl	671	21	2.1	161	4	US-09-621-976-16389	Sequence 16389, A
C 599	21	2.1	60	4	US-09-621-976-9432	Sequence 9432, Ap	672	21	2.1	162	4	US-09-621-976-10766	Sequence 10766, A
C 600	21	2.1	67	3	US-09-620-958A-6	Sequence 6, Appl	673	21	2.1	166	4	US-09-621-976-15316	Sequence 15316, A
C 601	21	2.1	75	4	US-09-621-976-12516	Sequence 12516, A	674	21	2.1	168	4	US-09-621-976-15316	Sequence 15316, A
C 602	21	2.1	80	4	US-09-284-627-15	Sequence 15, Appl	675	21	2.1	168	4	US-09-621-976-16870	Sequence 16870, A
C 603	21	2.1	81	4	US-09-621-976-9671	Sequence 9671, Ap	676	21	2.1	171	2	US-08-799-464A-34	Sequence 34, Appl
C 604	21	2.1	85	4	US-09-621-976-14741	Sequence 14741, A	677	21	2.1	173	4	US-09-621-976-9851	Sequence 9851, Ap
C 605	21	2.1	91	4	US-09-621-976-14925	Sequence 14925, A	678	21	2.1	173	4	US-09-621-976-15319	Sequence 15319, A
C 606	21	2.1	92	1	US-08-120-827-94	Sequence 94, Appl	679	21	2.1	176	4	US-09-621-976-11161	Sequence 11161, A
C 607	21	2.1	92	1	US-08-478-675-94	Sequence 94, Appl	680	21	2.1	178	4	US-09-621-976-15322	Sequence 15322, A
C 608	21	2.1	94	4	US-09-621-976-112471	Sequence 12471, A	681	21	2.1	179	4	US-09-621-976-16872	Sequence 16872, A
C 609	21	2.1	97	2	US-08-663-688A-5	Sequence 5, Appl	682	21	2.1	180	4	US-09-621-976-15320	Sequence 15320, A
C 610	21	2.1	100	4	US-09-621-976-12774	Sequence 12774, A	683	21	2.1	182	4	US-09-621-976-16971	Sequence 16971, A
C 611	21	2.1	104	2	US-08-803-899-8	Sequence 8, Appl	684	21	2.1	183	4	US-09-621-976-13606	Sequence 13606, A

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686	21	2.1	184	4	US-09-621-976-14731	Sequence 14731, A	759	21	2.1	276	4	US-09-621-976-15760	Sequence 15760, A
687	21	2.1	184	4	US-09-621-976-13418	Sequence 13418, A	760	21	2.1	277	3	US-09-007-005-3	Sequence 3, Appli
688	21	2.1	187	4	US-09-621-976-10364	Sequence 10364, A	761	21	2.1	277	3	US-09-244-796-3	Sequence 3, Appli
689	21	2.1	189	4	US-09-621-976-16457	Sequence 16457, A	762	21	2.1	278	4	US-09-370-838-159	Sequence 159, App
690	21	2.1	191	4	US-09-621-976-9596	Sequence 10184, A	763	21	2.1	278	4	US-09-621-976-10220	Sequence 10220, A
691	21	2.1	194	4	US-09-621-976-9596	Sequence 9596, Ap	764	21	2.1	279	4	US-09-621-976-2841	Sequence 2841, Ap
692	21	2.1	194	4	US-09-621-976-15317	Sequence 15317, A	765	21	2.1	284	4	US-09-621-976-2901	Sequence 2901, Ap
693	21	2.1	195	4	US-09-621-976-15314	Sequence 15314, A	766	21	2.1	284	4	US-09-621-976-3119	Sequence 3119, Ap
694	21	2.1	207	4	US-09-621-976-16455	Sequence 16455, A	767	21	2.1	286	4	US-09-621-976-17236	Sequence 17236, A
695	21	2.1	208	1	US-08-686-878A-37	Sequence 37, Appl	768	21	2.1	289	3	US-09-007-005-17	Sequence 17, Appl
696	21	2.1	208	4	US-09-175-928-37	Sequence 37, Appl	769	21	2.1	289	3	US-09-244-796-17	Sequence 17, Appl
697	21	2.1	210	4	US-09-621-976-15313	Sequence 15313, A	770	21	2.1	289	4	US-09-621-976-10009	Sequence 10009, A
698	21	2.1	212	4	US-09-621-976-1325	Sequence 1325, Ap	771	21	2.1	293	4	US-09-621-976-10686	Sequence 10686, A
699	21	2.1	214	4	US-09-621-976-9843	Sequence 9843, Ap	772	21	2.1	299	4	US-09-621-976-10211	Sequence 10211, A
700	21	2.1	215	4	US-09-621-976-15321	Sequence 15321, A	773	21	2.1	300	4	US-09-205-258-143	Sequence 143, App
701	21	2.1	216	1	US-08-686-878A-34	Sequence 34, Appl	774	21	2.1	300	4	US-09-621-976-16139	Sequence 16139, A
702	21	2.1	216	4	US-09-175-928-34	Sequence 34, Appl	775	21	2.1	300	4	US-09-621-976-17556	Sequence 17556, A
703	21	2.1	216	4	US-09-621-976-14957	Sequence 14957, A	776	21	2.1	301	4	US-09-621-976-16130	Sequence 16130, A
704	21	2.1	218	4	US-09-228-302-1	Sequence 1, Appli	777	21	2.1	306	4	US-09-621-976-16132	Sequence 16132, A
705	21	2.1	219	1	US-08-702-080-3	Sequence 3, Appli	778	21	2.1	307	4	US-09-621-976-16030	Sequence 16030, A
706	21	2.1	219	2	US-08-858-830-3	Sequence 3, Appli	779	21	2.1	310	4	US-09-621-976-16133	Sequence 16133, A
707	21	2.1	219	2	US-08-858-834-3	Sequence 3, Appli	780	21	2.1	310	4	US-09-621-976-16134	Sequence 16134, A
708	21	2.1	222	3	US-08-481-190-15	Sequence 15, Appl	781	21	2.1	312	4	US-09-621-976-11069	Sequence 11069, A
709	21	2.1	222	5	PCT-US93-00869-15	Sequence 15, Appl	782	21	2.1	314	3	US-09-277-016-37	Sequence 37, Appl
710	21	2.1	223	4	US-09-792-534-11	Sequence 11, Appl	783	21	2.1	314	4	US-09-883-548-7	Sequence 7, Appli
711	21	2.1	223	4	US-09-621-976-10791	Sequence 10791, A	784	21	2.1	314	4	US-09-883-717-7	Sequence 7, Appli
712	21	2.1	229	4	US-09-702-705-195	Sequence 195, App	785	21	2.1	314	4	US-09-757-949-7	Sequence 7, Appli
713	21	2.1	229	4	US-09-736-457-195	Sequence 195, App	786	21	2.1	319	2	US-08-244-537-11	Sequence 11, Appl
714	21	2.1	229	4	US-09-614-124B-195	Sequence 195, App	787	21	2.1	319	4	US-09-621-976-16129	Sequence 16129, A
715	21	2.1	229	4	US-09-621-976-10914	Sequence 10914, A	788	21	2.1	321	1	US-08-171-385-22	Sequence 22, Appl
716	21	2.1	229	4	US-09-671-325-195	Sequence 195, App	789	21	2.1	321	3	US-08-361-441B-22	Sequence 22, Appl
717	21	2.1	229	4	US-08-588-184-195	Sequence 195, App	790	21	2.1	322	4	US-09-621-976-16142	Sequence 16142, A
718	21	2.1	230	4	US-09-621-976-12495	Sequence 1495, A	791	21	2.1	323	4	US-09-621-976-10374	Sequence 10374, A
719	21	2.1	231	4	US-09-621-976-16456	Sequence 16456, A	792	21	2.1	323	4	US-09-621-976-16131	Sequence 16131, A
720	21	2.1	233	4	US-09-621-976-16429	Sequence 14629, A	793	21	2.1	327	4	US-09-621-976-16141	Sequence 16141, A
721	21	2.1	233	4	US-09-621-976-16873	Sequence 16873, A	794	21	2.1	330	3	US-09-078-294-24	Sequence 24, Appl
722	21	2.1	240	1	US-08-628-417-6	Sequence 6, Appli	795	21	2.1	334	2	US-08-522-421-3	Sequence 3, Appli
723	21	2.1	241	4	US-09-621-976-17071	Sequence 17071, A	796	21	2.1	336	4	US-09-621-976-2150	Sequence 2150, Ap
724	21	2.1	242	4	US-09-621-976-18328	Sequence 18328, A	797	21	2.1	338	4	US-09-621-976-2886	Sequence 2886, Ap
725	21	2.1	243	4	US-09-621-976-17624	Sequence 17624, A	798	21	2.1	340	1	US-08-171-385-27	Sequence 27, Appl
726	21	2.1	245	4	US-09-149-476-70	Sequence 70, Appl	799	21	2.1	340	3	US-08-361-441B-27	Sequence 27, Appl
727	21	2.1	247	1	US-08-691-641-4	Sequence 4, Appli	800	21	2.1	341	4	US-09-621-976-16135	Sequence 16135, A
728	21	2.1	249	4	US-09-621-976-10306	Sequence 10306, A	801	21	2.1	343	4	US-09-621-976-16603	Sequence 16603, A
729	21	2.1	250	4	US-09-621-976-10237	Sequence 10237, A	802	21	2.1	345	1	US-08-171-385-20	Sequence 20, Appl
730	21	2.1	250	4	US-09-621-976-10608	Sequence 10608, A	803	21	2.1	345	3	US-08-361-441B-20	Sequence 20, Appl
731	21	2.1	252	4	US-09-621-976-10239	Sequence 10239, A	804	21	2.1	347	1	US-08-104-072B-2	Sequence 2, Appli
732	21	2.1	252	4	US-09-621-976-10278	Sequence 10278, A	805	21	2.1	347	4	US-09-621-976-16136	Sequence 16136, A
733	21	2.1	255	4	US-09-480-921B-26	Sequence 26, Appl	806	21	2.1	348	4	US-09-621-976-13740	Sequence 13740, A
734	21	2.1	255	4	US-09-621-976-9406	Sequence 9406, Ap	807	21	2.1	349	1	US-07-603-451A-4	Sequence 4, Appli
735	21	2.1	255	4	US-09-621-976-10185	Sequence 10185, A	808	21	2.1	349	1	US-08-060-822A-4	Sequence 4, Appli
736	21	2.1	255	4	US-09-621-976-18743	Sequence 18743, A	809	21	2.1	349	4	US-09-105-542A-6	Sequence 6, Appli
737	21	2.1	257	3	US-09-385-982-370	Sequence 370, App	810	21	2.1	349	5	PCT-US94-05257-4	Sequence 4, Appli
738	21	2.1	257	4	US-09-621-976-2957	Sequence 2957, Ap	811	21	2.1	350	1	US-08-171-385-14	Sequence 14, Appl
739	21	2.1	257	4	US-09-621-976-10203	Sequence 10203, A	812	21	2.1	350	1	US-08-248-016-11	Sequence 11, Appl
740	21	2.1	258	4	US-09-621-976-15353	Sequence 15353, A	813	21	2.1	350	1	US-08-451-501-11	Sequence 11, Appl
741	21	2.1	259	4	US-09-621-976-15741	Sequence 15741, A	814	21	2.1	350	5	PCT-US95-06761-11	Sequence 11, Appl
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743	21	2.1	261	4	US-09-621-976-18330	Sequence 18330, A	816	21	2.1	351	4	US-09-621-976-15134	Sequence 15134, A
744	21	2.1	263	4	US-09-621-976-15330	Sequence 15330, A	817	21	2.1	351	4	US-09-621-976-16140	Sequence 16140, A
745	21	2.1	264	4	US-09-621-976-9577	Sequence 9577, Ap	818	21	2.1	355	4	US-09-621-976-16598	Sequence 16598, A
746	21	2.1	266	4	US-09-621-976-10269	Sequence 10269, A	819	21	2.1	358	4	US-09-621-976-927	Sequence 927, App
747	21	2.1	266	4	US-09-621-976-16933	Sequence 16933, A	820	21	2.1	361	2	US-08-465-380-39	Sequence 39, Appl
748	21	2.1	268	4	US-09-621-976-2415	Sequence 2415, Ap	821	21	2.1	361	2	US-08-486-397-39	Sequence 39, Appl
749	21	2.1	269	4	US-09-621-976-2903	Sequence 2903, Ap	822	21	2.1	361	2	US-08-486-399-39	Sequence 39, Appl
750	21	2.1	271	4	US-09-621-976-2960	Sequence 2960, Ap	823	21	2.1	361	2	US-08-461-965-39	Sequence 39, Appl
751	21	2.1	271	4	US-09-621-976-10153	Sequence 10153, A	824	21	2.1	361	2	US-08-634-641-39	Sequence 39, Appl
752	21	2.1	271	4	US-09-621-976-15737	Sequence 15737, A	825	21	2.1	361	3	US-08-249-471-39	Sequence 39, Appl
753	21	2.1	272	4	US-09-621-976-2953	Sequence 2953, Ap	826	21	2.1	361	3	US-08-249-472-39	Sequence 39, Appl
754	21	2.1	272	4	US-09-621-976-2988	Sequence 2988, Ap	827	21	2.1	361	3	US-08-249-451-39	Sequence 39, Appl
755	21	2.1	272	4	US-09-621-976-8353	Sequence 8353, Ap	828	21	2.1	361	3	US-08-809-455-39	Sequence 39, Appl
756	21	2.1	272	4	US-09-621-976-13581	Sequence 13581, A	829	21	2.1	361	3	US-09-249-461-39	Sequence 39, Appl
757	21	2.1	273	4	US-09-621-976-11078	Sequence 11078, A	830	21	2.1	361	3	US-09-249-448-39	Sequence 39, Appl

C 831	21	2.1	361	4	US-09-249-473-39	Sequence 39, Appl	904	21	2.1	437	4	US-09-542-615A-74	Sequence 74, Appl
C 832	21	2.1	371	4	US-09-621-976-19223	Sequence 19223, A	905	21	2.1	437	4	US-09-606-421B-74	Sequence 74, Appl
C 833	21	2.1	373	4	US-09-091-725-42	Sequence 42, Appl	906	21	2.1	437	4	US-09-621-976-17548	Sequence 17548, A
C 834	21	2.1	373	4	US-09-300-958A-15	Sequence 15, Appl	907	21	2.1	437	4	US-09-621-976-17548	Sequence 17548, A
C 835	21	2.1	373	4	US-09-385-982-494	Sequence 494, Appl	908	21	2.1	442	4	US-09-372-422A-35	Sequence 35, Appl
C 836	21	2.1	374	3	US-09-946-026-23	Sequence 23, Appl	909	21	2.1	442	4	US-09-288-143-41	Sequence 41, Appl
C 837	21	2.1	375	3	US-09-946-026-23	Sequence 23, Appl	910	21	2.1	442	4	US-09-288-143-41	Sequence 41, Appl
C 838	21	2.1	376	4	US-09-220-132-128	Sequence 128, Appl	911	21	2.1	450	4	US-09-703-457-388	Sequence 388, App
C 839	21	2.1	377	4	US-09-621-976-18854	Sequence 18854, A	912	21	2.1	450	4	US-09-736-457-388	Sequence 388, App
C 840	21	2.1	378	4	US-09-621-976-15461	Sequence 15461, A	913	21	2.1	450	4	US-09-614-124B-388	Sequence 388, App
C 841	21	2.1	383	4	US-09-621-976-17965	Sequence 17965, A	914	21	2.1	450	4	US-09-621-976-18072	Sequence 18072, A
C 842	21	2.1	383	4	US-09-621-976-17965	Sequence 17965, A	915	21	2.1	450	4	US-09-621-976-18072	Sequence 18072, A
C 843	21	2.1	385	4	US-09-688-988-47	Sequence 47, Appl	916	21	2.1	458	1	US-09-589-184-388	Sequence 388, App
C 844	21	2.1	385	4	US-09-621-976-12486	Sequence 12486, A	917	21	2.1	458	1	US-09-589-184-388	Sequence 388, App
C 845	21	2.1	388	4	US-09-621-976-18573	Sequence 18573, A	918	21	2.1	463	4	US-09-524-757-1	Sequence 1, Appl
C 846	21	2.1	391	4	US-09-621-976-18858	Sequence 18858, A	919	21	2.1	463	4	US-09-524-757-1	Sequence 1, Appl
C 847	21	2.1	393	4	US-09-439-313-357	Sequence 357, App	920	21	2.1	463	4	US-09-621-976-1544	Sequence 1544, App
C 848	21	2.1	393	4	US-09-352-616A-357	Sequence 357, App	921	21	2.1	463	4	US-09-621-976-1544	Sequence 1544, App
C 849	21	2.1	393	4	US-09-636-215-357	Sequence 357, App	922	21	2.1	467	4	US-09-328-475C-122	Sequence 122, App
C 850	21	2.1	393	4	US-09-685-166A-357	Sequence 357, App	923	21	2.1	467	4	US-09-328-475C-122	Sequence 122, App
C 851	21	2.1	395	2	US-09-630-822A-84	Sequence 84, Appl	924	21	2.1	467	4	US-09-621-976-3668	Sequence 2632, App
C 852	21	2.1	396	2	US-09-005-069-84	Sequence 84, Appl	925	21	2.1	470	4	US-09-621-976-3668	Sequence 2632, App
C 853	21	2.1	396	4	US-09-171-156A-33	Sequence 33, Appl	926	21	2.1	470	4	US-09-621-976-3668	Sequence 2632, App
C 854	21	2.1	396	4	US-09-004-730A-33	Sequence 33, Appl	927	21	2.1	472	4	US-09-621-976-3668	Sequence 2632, App
C 855	21	2.1	396	4	US-09-495-050A-98	Sequence 98, Appl	928	21	2.1	472	4	US-09-621-976-3668	Sequence 2632, App
C 856	21	2.1	396	4	US-09-981-799A-33	Sequence 33, Appl	929	21	2.1	472	4	US-09-621-976-3668	Sequence 2632, App
C 857	21	2.1	396	4	US-09-640-173-10	Sequence 10, Appl	930	21	2.1	475	3	US-09-621-976-3668	Sequence 2632, App
C 858	21	2.1	396	4	US-09-640-173-18	Sequence 18, Appl	931	21	2.1	475	3	US-09-621-976-3668	Sequence 2632, App
C 859	21	2.1	396	4	US-09-640-173-53	Sequence 53, Appl	932	21	2.1	476	4	US-09-621-976-3668	Sequence 2632, App
C 860	21	2.1	396	4	US-09-640-173-125	Sequence 125, App	933	21	2.1	476	4	US-09-621-976-3668	Sequence 2632, App
C 861	21	2.1	396	4	US-09-640-173-129	Sequence 129, App	934	21	2.1	476	4	US-09-621-976-3668	Sequence 2632, App
C 862	21	2.1	396	4	US-09-713-550-10	Sequence 10, Appl	935	21	2.1	476	4	US-09-621-976-3668	Sequence 2632, App
C 863	21	2.1	396	4	US-09-713-550-18	Sequence 18, Appl	936	21	2.1	476	4	US-09-621-976-3668	Sequence 2632, App
C 864	21	2.1	396	4	US-09-713-550-42	Sequence 42, Appl	937	21	2.1	476	4	US-09-621-976-3668	Sequence 2632, App
C 865	21	2.1	396	4	US-09-713-550-53	Sequence 53, Appl	938	21	2.1	476	4	US-09-621-976-3668	Sequence 2632, App
C 866	21	2.1	396	4	US-09-713-550-125	Sequence 125, App	939	21	2.1	476	4	US-09-621-976-3668	Sequence 2632, App
C 867	21	2.1	396	4	US-09-713-550-129	Sequence 129, App	940	21	2.1	476	4	US-09-621-976-3668	Sequence 2632, App
C 868	21	2.1	396	4	US-09-621-976-19065	Sequence 19065, A	941	21	2.1	480	4	US-09-621-976-3668	Sequence 2632, App
C 869	21	2.1	397	4	US-09-621-976-18071	Sequence 18071, A	942	21	2.1	480	4	US-09-621-976-3668	Sequence 2632, App
C 870	21	2.1	398	4	US-09-904-615-62	Sequence 62, Appl	943	21	2.1	480	4	US-09-621-976-3668	Sequence 2632, App
C 871	21	2.1	398	1	US-07-885-970A-13	Sequence 13, Appl	944	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 872	21	2.1	399	1	US-08-298-687A-13	Sequence 13, Appl	945	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 873	21	2.1	399	1	US-08-530-797-12	Sequence 12, Appl	946	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 874	21	2.1	399	1	US-08-298-829-13	Sequence 13, Appl	947	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 875	21	2.1	399	2	US-08-787-335-12	Sequence 12, Appl	948	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 876	21	2.1	400	4	US-08-956-171E-2132	Sequence 2132, App	949	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 877	21	2.1	403	4	US-09-621-976-18962	Sequence 18962, A	950	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 878	21	2.1	407	4	US-09-621-976-16714	Sequence 16714, A	951	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 879	21	2.1	408	4	US-09-222-575-43	Sequence 43, Appl	952	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 880	21	2.1	408	4	US-09-389-681-43	Sequence 43, Appl	953	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 881	21	2.1	408	4	US-09-620-405B-43	Sequence 43, Appl	954	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 882	21	2.1	408	4	US-09-339-338-43	Sequence 43, Appl	955	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 883	21	2.1	408	4	US-09-433-826B-43	Sequence 43, Appl	956	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 884	21	2.1	408	4	US-09-604-287A-43	Sequence 43, Appl	957	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 885	21	2.1	408	4	US-09-285-480-43	Sequence 43, Appl	958	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 886	21	2.1	408	4	US-09-834-739-43	Sequence 43, Appl	959	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 887	21	2.1	413	2	US-09-014-969-5	Sequence 5, Appl	960	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 888	21	2.1	413	4	US-09-621-976-16710	Sequence 16710, A	961	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 889	21	2.1	422	4	US-09-764-325A-3	Sequence 3, Appl	962	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 890	21	2.1	422	4	US-09-913-935-3	Sequence 3, Appl	963	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 891	21	2.1	424	4	US-09-621-976-11043	Sequence 11043, A	964	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 892	21	2.1	425	4	US-09-621-976-15712	Sequence 15712, A	965	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 893	21	2.1	425	4	US-09-621-976-15712	Sequence 15712, A	966	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 894	21	2.1	430	4	US-09-621-976-16711	Sequence 16711, A	967	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 895	21	2.1	435	3	US-09-385-982-518	Sequence 518, App	968	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 896	21	2.1	436	4	US-09-439-313-353	Sequence 353, App	969	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 897	21	2.1	436	4	US-09-352-616A-353	Sequence 353, App	970	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 898	21	2.1	436	4	US-09-636-215-353	Sequence 353, App	971	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 899	21	2.1	436	4	US-09-685-166A-353	Sequence 353, App	972	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 900	21	2.1	437	3	US-09-040-984-74	Sequence 74, Appl	973	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 901	21	2.1	437	4	US-09-123-912-74	Sequence 74, Appl	974	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 902	21	2.1	437	4	US-09-643-597-74	Sequence 74, Appl	975	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App
C 903	21	2.1	437	4	US-09-480-884A-74	Sequence 74, Appl	976	21	2.1	482	3	US-09-621-976-3668	Sequence 2632, App

977 21 2.1 536 4 US-09-643-597-70
978 21 2.1 536 4 US-09-480-884A-70
979 21 2.1 536 4 US-09-542-615A-70
980 21 2.1 536 4 US-09-608-421B-70
981 21 2.1 536 4 US-09-221-107-70
982 21 2.1 540 4 US-09-313-434C-15
983 21 2.1 543 4 US-09-904-615-33
984 21 2.1 548 4 US-09-186-276B-51
985 21 2.1 548 4 US-08-842-445-51
986 21 2.1 548 4 US-09-185-188B-51
987 21 2.1 552 4 US-09-621-976-2737
988 21 2.1 554 4 US-09-696-169A-14
989 21 2.1 557 4 US-09-439-313-384
990 21 2.1 557 4 US-09-352-616A-384
991 21 2.1 557 4 US-09-636-215-384
992 21 2.1 557 4 US-09-685-166A-384
993 21 2.1 565 4 US-09-583-733C-6
994 21 2.1 566 1 US-08-211-942-10
995 21 2.1 568 1 US-08-582-257-20
996 21 2.1 568 2 US-08-582-298-20
997 21 2.1 569 3 US-09-328-111-561
998 21 2.1 570 1 US-07-822-966B-1
999 21 2.1 572 4 US-09-696-169A-12
1000 21 2.1 572 4 US-09-424-978B-32

ALIGNMENTS

RESULT 1
US-08-671-320-15
; Sequence 16, Application US/08671320
; Patent No. 5840558
; GENERAL INFORMATION:
; APPLICANT: VIERLING JR., RICHARD A
; TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
; ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: 1125 SO. 103RD STREET
; STREET: SUITE 330
; CITY: OMAHA
; STATE: NE
; COUNTRY: US
; ZIP: 68124-1076

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/671,320
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JONDLE, ROBERT J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: 1227-001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-398-9000
TELEFAX: 402-398-9005
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..38
FEATURE:
NAME/KEY: CDS

; LOCATION: 39..977
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 978..1167
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 39..101
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 102..977
US-08-671-320-16

Query Match 2.7%; Score 27; DB 2; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TTTTGATATAAAAAAAAAAAAAAAAAAAAA 982
|||||
Db 1139 TTTTGATATAAAAAAAAAAAAAAAAAAAAA 1165

RESULT 2
US-08-868-577-16
; Sequence 16, Application US/08868577
; Patent No. 586695
; GENERAL INFORMATION:
; APPLICANT: Vierling Jr., Richard A

; TITLE OF INVENTION: A SOYBEAN PEROXIDASE GENE FAMILY AND AN
; ASSAY FOR DETECTING SOYBEAN PEROXIDASE ACTIVITY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: 555 13th Street NW, Suite 701 East
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/868,577
FILING DATE: 04-JUN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jondle, Robert J.
REGISTRATION NUMBER: 33,915
REFERENCE/DOCKET NUMBER: N1227-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 402-333-1550
TELEFAX: 402-333-1510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..38
FEATURE:
NAME/KEY: CDS
LOCATION: 39..977
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 978..1167
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 39..101
FEATURE:

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; NAME/KEY: mat_peptide
; LOCATION: 102..977
US-08-868-577-16

Query Match      2.7%; Score 27; DB 2; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TTTTGATAAAAAAAAAAAAAAAAAAAAAA 982
DB 1139 TTTTGATAAAAAAAAAAAAAAAAAAAAAA 1165

RESULT 3
US-09-207-914-16
; Sequence 16, Application US/09207914A
; Patent No. 6586593
; GENERAL INFORMATION:
; APPLICANT: Vierling Jr., Richard A.
; TITLE OF INVENTION: A Soybean Peroxidase Gene Family and an Assay for
; FILE REFERENCE: Detecting Soybean Peroxidase Activity
; CURRENT APPLICATION NUMBER: US/09/207,914A
; CURRENT FILING DATE: 1998-12-09
; EARLIER APPLICATION NUMBER: US 08/868,577
; EARLIER FILING DATE: 1997-06-04
; EARLIER APPLICATION NUMBER: US 08/671,320
; EARLIER FILING DATE: 1995-10-27
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(38)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(977)
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: (987)..(1167)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (39)..(101)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (102)..(977)
US-09-207-914-16

Query Match      2.7%; Score 27; DB 4; Length 1167;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 956 TTTTGATAAAAAAAAAAAAAAAAAAAAAA 982
DB 1139 TTTTGATAAAAAAAAAAAAAAAAAAAAAA 1165

RESULT 4
US-08-651-136C-7
; Sequence 7, Application US/08651136C
; Patent No. 6001639
; GENERAL INFORMATION:
; APPLICANT: Schuelein, Martin
; APPLICANT: Andersen, Lene N.
; APPLICANT: Lassen, Soren F.
; APPLICANT: Kauppinen, Markus S.
; APPLICANT: Lange, Lene
; APPLICANT: Nielsen, Ruby I.
; APPLICANT: Ihara, Michiko
; APPLICANT: Takagi, Shinobu

```

```

; TITLE OF INVENTION: No. 6001639el Endoglucanases
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6001639o No. 6001639disk of No. 6001639th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/651,136C
; FILING DATE: 21-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4366.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1154 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 51..935
US-08-651-136C-7

Query Match      2.8%; Score 26; DB 3; Length 1154;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 957 TTTGATAAAAAAAAAAAAAAAAAAAAAA 982
DB 1091 TTTGATAAAAAAAAAAAAAAAAAAAAAA 1116

RESULT 5
US-09-229-911A-7
; Sequence 7, Application US/09229911A
; Patent No. 6387690
; GENERAL INFORMATION:
; APPLICANT: Schuelein, Martin
; APPLICANT: Andersen, Lene N.
; APPLICANT: Lassen, Soren F.
; APPLICANT: Kauppinen, Markus S.
; APPLICANT: Lange, Lene
; APPLICANT: Nielsen, Ruby I.
; APPLICANT: Ihara, Michiko
; APPLICANT: Takagi, Shinobu
; TITLE OF INVENTION: No. 6387690el Endoglucanases
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6387690o No. 6387690disk of No. 6387690th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/229,911A
 ; FILING DATE: 13-Jan-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/651,136
 ; FILING DATE: 21-MAY-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lambiris, Elias J.
 ; REGISTRATION NUMBER: 33,728
 ; REFERENCE/DOCKET NUMBER: 4366.200-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1154 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 51..935
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-09-229-911A-7

Query Match 2.6%; Score 26; DB 4; Length 1154;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 957 TTGATATAAAAAAAAAAAAAAAAAAAAA 982
 Db 1091 TTGATATAAAAAAAAAAAAAAAAAAAAA 1116

RESULT 6
 5188642-3
 ; Patent No. 5188642
 ; APPLICANT: SHAH, DILIP M.; ROGERS, STEPHEN G.; HORSCH, ROBERT B.
 ; FRALEY, ROBERT T.
 ; TITLE OF INVENTION: GLYPHOSPHATE-RESISTENT PLANTS
 ; NUMBER OF SEQUENCES: 16
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/478,794
 ; FILING DATE: 12-FEB-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 879,814
 ; FILING DATE: 7-JUL-1986
 ; APPLICATION NUMBER: 792,390
 ; FILING DATE: 29-OCT-1985
 ; APPLICATION NUMBER: 763,482
 ; FILING DATE: 07-AUG-1985
 ; SEQ ID NO: 3:
 ; LENGTH: 1978
 5188642-3

Query Match 2.6%; Score 26; DB 6; Length 1978;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 957 TTGATATAAAAAAAAAAAAAAAAAAAAA 982
 Db 1939 TTGATATAAAAAAAAAAAAAAAAAAAAA 1964

RESULT 7
 US-09-640-173-77/c
 ; Sequence 77, Application US/09640173
 ; Patent No. 6613515
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Stolk, John A.

; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
 ; TITLE OF INVENTION: METHODS OF USE THEREFOR
 ; FILE REFERENCE: 210121.484C2
 ; CURRENT APPLICATION NUMBER: US/09/640,173
 ; CURRENT FILING DATE: 2000-08-15
 ; NUMBER OF SEQ ID NOS: 196
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 77
 ; LENGTH: 396
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(396)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-640-173-77

Query Match 2.5%; Score 25; DB 4; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.065;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 958 TTGATATAAAAAAAAAAAAAAAAAAAAA 982
 Db 36 TTGATATAAAAAAAAAAAAAAAAAAAAA 12

RESULT 8
 US-09-713-550-77/c
 ; Sequence 77, Application US/09713550
 ; Patent No. 6617109
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Stolk, John A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.484C4
 ; CURRENT APPLICATION NUMBER: US/09/713,550
 ; CURRENT FILING DATE: 2000-11-14
 ; NUMBER OF SEQ ID NOS: 205
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 77
 ; LENGTH: 396
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(396)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-713-550-77

Query Match 2.5%; Score 25; DB 4; Length 396;
 Best Local Similarity 100.0%; Pred. No. 0.065;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 958 TTGATATAAAAAAAAAAAAAAAAAAAAA 982
 Db 36 TTGATATAAAAAAAAAAAAAAAAAAAAA 12

RESULT 9
 US-08-893-654B-5
 ; Sequence 5, Application US/08893654B
 ; Patent No. 6165748
 ; GENERAL INFORMATION:
 ; APPLICANT: RACIE, LISA, ET ALIA
 ; TITLE OF INVENTION: FRAZZLED NUCLEOTIDE SEQUENCES,
 ; TITLE OF INVENTION: EXPRESSION PRODUCTS, COMPOSITIONS AND USES
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESS: GENETICS INSTITUTE, INC.
 ; STREET: 87 CAMBRIDGE PARK DRIVE
 ; CITY: CAMBRIDGE
 ; STATE: MA


```

; GENERAL INFORMATION:
; APPLICANT: Kennedy, Jacqueline
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: PURIFIED MAMMALIAN T CELL ANTIGENS AND
; TITLE OF INVENTION: RELATED REAGENTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,742
; FILING DATE: 26-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0505
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1940 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1197
;
US-08-429-742-3

Query Match 2.5%; Score 25; DB 1; Length 1940;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 25; Conservative 0; Mismatches 0; Indels

QY 958 TTGATAAAAAAAAAAAAAAAAAAAAAA 982
DB 1909 TTGATAAAAAAAAAAAAAAAAAAAAAA 1933

RESULT 12
US-09-162-021B-1
; Sequence 1, Application US/09162021B
; Patent No. 6337391
; GENERAL INFORMATION:
; APPLICANT: H. William Harris
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
; TITLE OF INVENTION: Species and Methods of Use thereof
; FILE REFERENCE: 2856.1001-007
; CURRENT APPLICATION NUMBER: US/09/162,021B
; CURRENT FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: PCT/US97/05031
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/622,738
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 27, 2004, 09:10:49 ; Search time 92.3848 Seconds
(without alignments)
709.543 Million cell updates/sec

Title: US-10-069-527-4

Perfect score: 1216

Sequence: 1 MARGKIEIKLIENQTNQVY.....RHGSSLSGSIITLHLRLA 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:**

1: Geneseq1980s:**

2: Geneseq1980s:**

3: Geneseq2000s:**

4: Geneseq2001s:**

5: Geneseq2002s:**

6: Geneseq2003as:**

7: Geneseq2003bs:**

8: Geneseq2004s:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1216	100.0	232	4	AU00187	Granny Sm
2	709.5	58.3	227	4	AAB68435	Amino aci
3	709.5	58.3	227	5	ABG30865	Poplar pr
4	709.5	58.3	227	7	ABU61893	Poplar ho
5	701.5	57.7	227	3	AAV58654	Poplar PT
6	641.5	52.8	231	2	AA433385	Product O
7	616.5	50.7	227	5	AAE25757	Soybean A
8	595.5	48.1	233	3	AAE25552	Eucalyptu
9	569	46.8	232	3	AAE25577	Arabidops
10	564	46.4	232	3	AAE25576	Arabidops
11	564	46.4	232	3	AAE254029	Arabidops
12	564	46.4	236	3	AAE254679	Arabidops
13	564	46.4	241	3	AAE254028	Arabidops
14	553.5	45.5	227	5	AAE25755	Corn AP3
15	548	45.1	224	5	AAE25763	Rice MAD3
16	488	40.1	171	3	AAE25218	Arabidops
17	488	40.1	181	3	AAE25217	Arabidops
18	419	34.5	108	3	AAE25227	Eucalyptu
19	410.5	33.8	195	3	AAE253164	Eucalyptu
20	364	29.9	186	3	AAE25578	Arabidops
21	359	29.5	186	3	AAE25578	Arabidops
22	355.5	29.2	215	4	AAU00186	Granny Sm
23	331.5	27.3	208	3	AAE21899	Arabidops
24	326	26.8	210	2	AA46555	fbpl, for
25	313.5	25.8	209	5	ABG60942	Novel flo

26	312.5	25.7	209	5	ABG60945	Novel flo
27	311.5	25.6	260	5	ABG60932	Novel flo
28	310.5	25.5	209	5	ABG60941	Novel flo
29	308.5	25.4	209	5	AAE25756	Corn AP3
30	305.5	25.1	240	4	AAE25756	Maize ZmM
31	305.5	25.1	240	4	AAE25756	Maize ZmM
32	305.5	25.1	240	4	AAE25756	Maize ZmM
33	305.5	25.1	240	4	AAE25756	Maize ZmM
34	296.5	24.4	221	3	AAE26345	Corn nitr
35	296.5	24.4	221	3	AAE26345	Corn nitr
36	295	24.3	241	2	AAE26345	Corn nitr
37	294.5	24.2	249	2	AAE26345	Corn nitr
38	293.5	24.1	260	5	AAE26345	Corn nitr
39	291	23.9	244	3	AAE26345	Corn nitr
40	290.5	23.9	238	5	AAE26345	Corn nitr
41	290.5	23.9	238	5	AAE26345	Corn nitr
42	290.5	23.9	238	5	AAE26345	Corn nitr
43	290	23.8	210	6	AAE26345	Corn nitr
44	289	23.8	205	5	AAE26345	Corn nitr
45	288.5	23.7	228	3	AAE26345	Corn nitr

ALIGNMENTS

RESULT 1
AAU00187
ID AAU00187 standard; peptide; 232 AA.

XX AAU00187;

XX AAU00187;

DT 11-SEP-2003 (revised)

DT 17-MAY-2001 (first entry)

XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

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XX AAU00187;

XX AAU00187;

XX AAU00187;

XX AAU00187;

CC for pre-selecting plants (mutated in MdPI, MdAP3 or their equivalents),
 CC for use in an accelerated breeding programme to produce seedless fruit.
 CC They may also be used in designing probes and primers for MdPI or MdAP3,
 CC or their variants. The seedless fruiting plant is more convenient than
 CC seeded fruit since these can be cropped without pollination, reducing
 CC dependence on bees, pollinator varieties and warm weather at flowering.
 CC The absence of pollen is also advantageous to alleviate environmental
 CC concerns regarding the transfer of transgenes to non-transgenic by cross
 CC pollination. Seedless cultivars can also avoid or reduce biennial bearing
 CC tendencies that have been attributed to the inhibition of flower bud
 CC formation by developing seeds and are less susceptible to codling moth
 CC compared to seeded fruit. (Updated on 11-SEP-2003 to standardise OS
 CC field)

XX SQ Sequence 232 AA;

Query Match 100.0%; Score 1216; DB 4; Length 232;
 Best Local Similarity 100.0%; Pred. No. 1.1e-105; Indels 0; Gaps 0;
 Matches 232; Conservative 0; Mismatches 0;

QY 1 MARGKIEIKLIENQTNROVTSYKRRNGIFPKAQELTVLCAKVSILMSNTNKMHEVISP 60
 DB 1 MARGKIEIKLIENQTNROVTSYKRRNGIFPKAQELTVLCAKVSILMSNTNKMHEVISP 60
 QY 61 TTTTSMYDDYQKTGIDLWRTHESMKDTLWKLKEINNKLRREIRQRLGHDNLGLSFDE 120
 DB 61 TTTTSMYDDYQKTGIDLWRTHESMKDTLWKLKEINNKLRREIRQRLGHDNLGLSFDE 120
 QY 121 LASLDEMOSSLDAIRQRYHVIKTQTETTKKKVKNLEQRGNMLHGVDQEAAGEDPQY 180
 DB 121 LASLDEMOSSLDAIRQRYHVIKTQTETTKKKVKNLEQRGNMLHGVDQEAAGEDPQY 180
 QY 181 GYEDNEGDEYSAALNSGANNLYTFHLHH-----PNLHGGSSIGSSITLHDLRLA 232
 DB 181 GYEDNEGDEYSAALNSGANNLYTFHLHH-----PNLHGGSSIGSSITLHDLRLA 232

RESULT 2
 AAB68435
 ID AAB68435 standard; protein; 227 AA.
 XX AAB68435;

XX 23-JUL-2001 (first entry)

XX Amino acid sequence of the floral homeotic protein PTD.

XX Floral homeotic gene; PDF; PRLP; PTAG-1; PTAG-2; floral tissue; LEAFY;
 KW LEY; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
 KW fertility; sterility.

XX Populus balsamifera.

XX Key Location/Qualifiers
 FH Domain 1..57
 FT Domain /note= "MADS domain"
 FT Domain 87..154
 FT Domain /note= "K-domain"

XX CA2319853-A1.

XX 01-APR-2001.

XX 02-OCT-2000; 2000CA-02319853.

XX 01-OCT-1999; 99US-00410464.

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX Rottman WH, Strauss SH, Brunner AM, Sheppard LA;

XX WPI; 2001-336098/36.

XX N-PSDB; AAF85391, AAF85392, AAF85393.

XX Novel isolated polynucleotide derived from Populus species, useful for
 PT producing transgenic plants having modified fertility characteristic,
 PT particularly sterility.

XX Claim 23; Page 43-44; 69pp; English.

XX The present sequence represents a floral homeotic protein, designated
 CC PDF. It is derived from Populus balsamifera subsp. trichocarpa. The
 CC specification also describes PRLP, PTAG-1 and PTAG-2 proteins. The floral
 CC homeotic proteins are expressed in floral tissues. PTLF is a homologue of
 CC LEAFY (LFY) and FLORICAULA (FLO), and is expressed in immature
 CC inflorescences on which floral primordia are developing. PTD is a
 CC homologue of DEFICIENS (DEF), and is strongly expressed in stamen
 CC primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are
 CC homologues of AGAMOUS (AG). The floral homeotic proteins and
 CC polynucleotides are useful for producing transgenic plants having
 CC modified fertility characteristics, particularly sterility

XX Sequence 227 AA;

Query Match 58.3%; Score 709.5; DB 4; Length 227;
 Best Local Similarity 62.3%; Pred. No. 3.6e-59;
 Matches 149; Conservative 24; Mismatches 45; Indels 21; Gaps 5;

QY 1 MARGKIEIKLIENQTNROVTSYKRRNGIFPKAQELTVLCAKVSILMSNTNKMHEVISP 60
 DB 1 MARGKIEIKLIENQTNROVTSYKRRNGIFPKAQELTVLCAKVSILMSNTNKMHEVISP 60
 QY 61 TTTTSMYDDYQKTGIDLWRTHESMKDTLWKLKEINNKLRREIRQRLGHDNLGLSFDE 120
 DB 61 TTTTSMYDDYQKTGIDLWRTHESMKDTLWKLKEINNKLRREIRQRLGHDNLGLSFDE 120
 QY 121 LASLDEMOSSLDAIRQRYHVIKTQTETTKKKVKNLEQRGNMLHGVDQEAAGEDPQY 180
 DB 121 LRGLQHEMTALNGVRGRKHVITQNETYRKKNLEERHGNLLMEY---EAKLEDQY 177
 QY 181 GYEDNEGDEYSAALNSGANNLYTFHLHH-----PNLHGGSSIGSSITLHDLRL 231
 DB 178 GLVDN----EAAVALANGASNLVAFRLHGHGHHHHLPNLHL-GDGFGA-----HEURL 226

RESULT 3

ABG30865

ID ABG30865 standard; protein; 227 AA.

XX AC ABG30865;

XX 29-AUG-2003 (revised)

DT 07-OCT-2002 (first entry)

XX Poplar protein transduction domain, PTD, protein.

XX Poplar; plant; DEFICIENS; transgenic; promoter;
 KW protein transduction domain; floral homeotic gene;
 KW floral-specific expression; cytotoxin; fertility; sterility; PTLF;
 KW PTAG-1; PTAG-2.

XX Populus balsamifera; subsp. trichocarpa.

XX Key Location/Qualifiers
 FH Domain 1..57
 FT Domain /label= "MADS domain"

FT /note= "MADS" is named for the first 4 proteins in which
 FT it was discovered, yeast minichromosome maintenance
 FT factor, floral homeotic genes AG and DEF and human serum
 FT response factor"
 FT 87..154
 FT Domain /label= "K-domain"

XX US6395892-B1.

XX 28-MAY-2002.

PD

XX 01-OCT-1999; 99US-00410464.
FF
XX 06-APR-1998; 98US-0080851P.
PR
XX 06-APR-1999; 99US-00287700.
PR
XX (UYOR-) UNIV OREGON HEALTH SCI.
PA
XX Strauss SH, Rottmann W, Brunner A, Sheppard L;
PI
XX WPI; 2002-572853/61.
DR
XX N-PSDB; ABK88484, ABK88485.
DR
XX New protein transduction domain promoter nucleic acid molecule useful for
PT producing transgenic plants having modified fertility characteristics,
PT particularly sterility.
XX
XX Disclosure; Col 39-42; 46pp; English.
PS
XX The invention relates to an isolated nucleic acid molecule especially a
XX protein transduction domain (PTD) promoter; (i) that hybridises under
XX wash conditions of 0.2 x SSC (saline sodium citrate), 0.1 % SDS (sodium
XX dodecyl sulphate) at 65 plus or to nucleotides or (ii) comprising 35
XX consecutive nucleotides of the PTD gene. PTD is a floral homeotic gene
XX and is the homologue of DEFICIENS. Also includes are a recombinant
XX nucleic acid comprising the PTD promoter, a cell transforming with the
XX recombinant nucleic acid and a transgenic plant comprising the
XX transduced cell. The PTD promoter is useful to obtain floral-specific
XX expression of genes such as cytotoxins, that are employed in genetic
XX ablation strategies to produce trees having modified fertility
XX characteristics, including sterility. Genetic constructs comprising
XX antisense versions or dominant negative mutants of PTD are useful in
XX producing genetically engineered Poplars and other trees, and for sense
XX suppression. Also disclosed are 3 other homeotic genes PTLF, PTAG-1 and
XX PTAG-2 (none are defined). The present sequence is the PTD protein.
XX (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 227 AA;
Query Match 58.3%; Score 709.5; DB 5; Length 227;
Best Local Similarity 62.3%; Pred. No. 3.6e-58;
Matches 149; Conservative 24; Mismatches 45; Indels 21; Gaps 5;
QY 1 MARGKIEIKLIENQTRQVTSKRNGIFPKAQLTFLCDKAVSLIMLNTNKHVEYISP 60
DB 1 MGRGKIEIKLIENPTNRQVTSKRNGIFPKAQLTFLCDKAVSLIMLNTNKLNEYISP 60
QY 61 TTTTSMYDDYQKTGIDLRWTHESKMDTLWLKKEINNKLRREIRORLGHDLNGLSFDE 120
DB 61 STSTKKIYDQYQNALGIDLMGTQYKMQEHLRLKNDINHKLQRIQRORRGEGLNLSIDH 120
QY 121 LASLDDMQSSLDIAIRQRYHYVKTQTETTTKKVKNLEORRGNMLHGYFDQEAAGDPQY 180
DB 121 LRGLQHMTEALNGVRGRKYHYVKTQNETYRKVKVKNLEERHGNLMLEY---EAKLEDQY 177
QY 181 GYEDNEGDEYESALNSGANNLYTFHLH-----PNLHGGSSIGSSITHLHLRL 231
DB 178 GLVDN-----EAAVALANGASNDYAPRLHGHNNHHLPNHL-GDGFGA-----HELR 226
RESULT 4
ID ABU61893
XX ABU61893 standard; protein; 227 AA.
XX AC ABU61893;
XX 18-AUG-2003 (first entry)
XX DE Poplar homeotic protein PTD.
XX KW Poplar; PTD; deficiencies; homeotic gene; floral development; sterile tree;
XX pulp; paper; plant.
XX

OS Populus balsamifera subsp. trichocarpa.
XX
XX Key Location/Qualifiers
FH 1..57
FT Domain /label= MADS_domain
FT Domain 87..154
FT Domain /label= K_domain
XX
XX US2003033628-A1.
XX
XX 13-FEB-2003.
XX
XX 21-MAR-2002; 2002US-00104580.
XX
XX 06-APR-1998; 98US-0080851P.
PR
XX 06-APR-1999; 99US-00287700.
PR
XX 01-OCT-1999; 99US-00410464.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
PA
XX Strauss SH, Rottmann W, Brunner A, Sheppard L;
PI
XX WPI; 2003-466273/44.
XX
XX N-PSDB; ACA62517, ACA62518.
DR
XX New floral homeotic nucleic acid molecules, useful for the manipulation
PT of flowering in Poplar and other plant species, and for producing
PT transgenic plants having modified fertility characteristics, particularly
PT sterility.
XX
XX Claim 23; Page 22; 48pp; English.
PS
XX The invention relates to an isolated nucleic acid molecule comprising at
XX least 15 consecutive nucleotides of the gene, cDNA or coding sequence of
XX 4 homeotic genes from poplar, PTLF (LEAFY and FLORICA homologue), PTD
XX (DEFICIENS homologue), and PTAG-1/PTAG-2 (both homologues of AGAMOUS).
XX Also included are a recombinant nucleic acid molecule comprising a
XX promoter sequence operably linked to the nucleic acid molecule, a cell
XX transformed with the nucleic acid molecule, a transgenic plant comprising
XX the recombinant nucleic acid molecule and the purified proteins encoded
XX by the nucleic acids. The nucleic acid molecules are useful for the
XX manipulation of flowering in Poplar and other plant species, for
XX producing transgenic plants having modified fertility characteristics
XX (particularly sterility) and in the pulp and paper industries. The
XX present sequence is the poplar PTD protein
XX
SQ Sequence 227 AA;
Query Match 58.3%; Score 709.5; DB 7; Length 227;
Best Local Similarity 62.3%; Pred. No. 3.6e-58;
Matches 149; Conservative 24; Mismatches 45; Indels 21; Gaps 5;
QY 1 MARGKIEIKLIENQTRQVTSKRNGIFPKAQLTFLCDKAVSLIMLNTNKHVEYISP 60
DB 1 MGRGKIEIKLIENPTNRQVTSKRNGIFPKAQLTFLCDKAVSLIMLNTNKLNEYISP 60
QY 61 TTTTSMYDDYQKTGIDLRWTHESKMDTLWLKKEINNKLRREIRORLGHDLNGLSFDE 120
DB 61 STSTKKIYDQYQNALGIDLMGTQYKMQEHLRLKNDINHKLQRIQRORRGEGLNLSIDH 120
QY 121 LASLDDMQSSLDIAIRQRYHYVKTQTETTTKKVKNLEORRGNMLHGYFDQEAAGDPQY 180
DB 121 LRGLQHMTEALNGVRGRKYHYVKTQNETYRKVKVKNLEERHGNLMLEY---EAKLEDQY 177
QY 181 GYEDNEGDEYESALNSGANNLYTFHLH-----PNLHGGSSIGSSITHLHLRL 231
DB 178 GLVDN-----EAAVALANGASNDYAPRLHGHNNHHLPNHL-GDGFGA-----HELR 226
RESULT 5
ID AAY58654
XX AAY58654 standard; protein; 227 AA.
XX

AC AAY58654;
 XX 11-APR-2000 (first entry)
 XX Poplar PTD floral homeotic gene-encoded protein.
 DE Poplar; PTD; floral homeotic gene; transgenic plant; sterility;
 KW fertility.
 XX Populus balsamifera subsp. trichocarpa.
 OS
 XX Key Location/Qualifiers
 FH Domain 1..60
 FT /note= "MADS domain"
 FT Domain 88..143
 FT /note= "K domain"
 XX CA2227940-A1.
 PN
 XX 06-OCT-1999.
 PD
 XX 07-APR-1998; 98CA-0227940.
 PF
 XX 06-APR-1998; 98US-00080851.
 PR
 XX (UYOR-) UNIV OREGON HEALTH SCI.
 PA
 XX Rottmann WH, Brunner AM, Sheppard LA, Strauss SH;
 PI
 XX WPI, 2000-106662/10.
 DR N-PSDB; AAZ57942, AAZ57943.
 XX
 XX Nucleic acid from Populus trichocarpa genes, useful for producing
 PT transgenic plants, particularly trees, with modified fertility
 PT characteristics such as sterility.
 XX
 PS Claim 31; Page 49-50; 92pp; English.
 XX

CC The present sequence is that of the novel PTD protein of poplar (Populus
 CC balsamifera subsp. trichocarpa), as deduced from newly isolated PTD gene
 CC and cDNA sequences (see AAZ57942-43). PTD is 1 of 4 novel floral homeotic
 CC genes identified in this poplar species. It is a homologue of DEFICIENS
 CC and is expressed strongly in stamen primordia from the onset of
 CC organogenesis, and is also expressed at low levels in carpel primordia.
 CC PTD contains both a MADS domain and a K-domain. The invention provides
 CC nucleic acid sequences of the 4 novel Populus genes, the corresponding
 CC cDNA sequences (see AAZ47942-49) and deduced amino acid sequences (see
 CC AAY58454-57). It also provides methods of using the gene and cDNA
 CC sequences to produce genetically engineered Populus and other trees
 CC having modified fertility characteristics, including sterility. Genetic
 CC constructs useful in producing genetically engineered Populus and other
 CC trees include antisense versions of PTD, dominant negative mutants, and
 CC constructs useful for sense suppression. Sterile trees allow increased
 CC wood yield and a reduction in the production of allergens such as pollen
 CC
 XX Sequence 227 AA;

Query Match 57.7%; Score 701.5; DB 3; Length 227;
 Best Local Similarity 61.5%; Pred. No. 28-57;
 Matches 147; Conservative 26; Mismatches 45; Indels 21; Gaps 5;
 QY 1 MARGKIEIKLIENQTNQVTSYKRRNGIFPKAQLTCLVCDKAVSLIMLNTNKGHYISP 60
 DB 1 MGRKIEIKLIENPTNQVTSYKRRNGIFPKAQLTCLVCDKAVSLIIVNTKNLEYISP 60
 QY 61 TTTTSMYDDYQKTMGIDLWRTHESKMDTLWLKKEINNKLRREIRORLGHDLNGLSFDE 120
 DB 61 STFTKTYDQYQALGIDLTGTYKQKQHLKRLNDINHKLROEIRQRGEGDLNLSIDH 120
 QY 121 LASLDDMQSSLDIAIRKQKHVIKTOTETTKKKVKNLEQRGNMLHGYFDQAAGEDPOY 180
 DB 121 LRGLQHQWTEALNGVRGKQKHVIKTQNETYRKVKVNLBEEHGNLNEY---EAKLEDROY 177

QY 181 GYEDNEGDYESALALNSGANNLYTFHLHH-----PNLHHGGSSLGSSITHLHLRL 231
 DB 178 GLVDN-----EAAVALANGASNDLYAPRLHHGHNHHHLNHL-GDGFGA-----HELRL 226
 RESULT 6
 AAR43385
 ID AAR43385 standard; protein; 231 AA.
 XX
 AC AAR43385;
 XX
 DT 25-MAR-2003 (revised)
 DT 19-JUN-1994 (first entry)
 XX
 DE Product of homeotic gene green petal.
 XX
 KW Plant; organ morphogenesis; control; petunia; petals.
 XX
 OS Petunia.
 XX WO9321322-A1.
 XX
 PD 28-OCT-1993.
 PF
 XX 13-APR-1993; 93WO-US003508.
 PR
 XX 13-APR-1992; 92US-00867580.
 PR 06-JUL-1992; 92US-00909589.
 XX
 XX (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Halfter U, Van Der Krol AR, Kush A, Chua N;
 XX
 DR WPI, 1993-351732/44.
 DR N-PSDB; AAQ51169.
 XX
 XX Plant organ morphogenesis control and determ. - by regulating the
 PT expression of homeotic genes which determine the identity of the organ.
 PS Disclosure; Fig 2; 74pp; English.

CC The homeotic gene green petal from petunia has been cloned and
 CC characterised previously. The gene was used in a new method for
 CC controlling the morphogenesis of plant organs comprising regulating the
 CC expression of the gene using ectopic expression. Such a method can be
 CC used to determine and control plant organ morphogenesis, such as
 CC modifying petals without altering the reproductive portions of the
 CC flower. See also AAR43386-7. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 XX Sequence 231 AA;

Query Match 52.8%; Score 641.5; DB 2; Length 231;
 Best Local Similarity 55.6%; Pred. No. 8.7e-52;
 Matches 129; Conservative 36; Mismatches 52; Indels 15; Gaps 4;
 QY 1 MARGKIEIKLIENQTNQVTSYKRRNGIFPKAQLTCLVCDKAVSLIMLNTNKGHYISP 60
 DB 1 MARGKIQIKRIENQTNQVTSYKRRNGIFPKANETLVCDKAVSIIMISSTGKLHEFISP 60
 QY 61 TTTTSMYDDYQKTMGIDLWRTHESKMDTLWLKKEINNKLRREIRORLGHDLNGLSFDE 120
 DB 61 SITTKQLFDLYQKTVGVLDLWNSHYEKQEQQLKKEVNRNLKEIRORMGESLNDLNEYQ 120
 QY 121 LASLDDMQSSLDIAIRKQKHVIKTOTETTKKKVKNLEQRGNMLHGYFDQAAGEDPOY 180
 DB 121 LEELMENVDNLSKLIREKQKVIQNETFKKKVNVVEIHRNLL-----LEFDARQEDP-Y 176
 QY 181 GYEDNEGDYESALALNSGANNLYTFHL-----HFNLHHGGSSLGSSIT 224
 DB 177 GLVQEGDYNSVLGFPNGGHRILALRQPNHQPNNHHHLHSG---GSDIT 225

RESULT 7
 AAE25757
 ID AAE25757 standard; protein; 227 AA.
 XX
 AC AAE25757;
 XX
 DT 04-NOV-2002 (first entry)
 XX
 DE Soybean AP3 homologue protein from clone sflin.pk001.116.
 XX
 KW Floral developmental protein; flowering locus T; APETALA3; transgenic;
 KW FT; AP3; transgenic plant; fertility; flower development; gene mapping;
 KW sterility; plant growth; inflorescence architecture; plant morphology;
 KW tissue culture; cell division; soybean.
 XX
 OS Glycine max.
 XX
 FN WO200244390-A2.
 XX
 PD 06-JUN-2002.
 XX
 XX 21-NOV-2001; 2001WO-US043750.
 PF
 XX 28-NOV-2000; 2000US-0253415P.
 PR
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA
 XX Cahoon EB, Cahoon RE, Klein TW, Rafalski AJ, Sakai H;
 PI
 XX WPI; 2002-547703/58.
 DR
 DR N-PSDB; AAD42259.
 XX
 XX New floral developmental polypeptide having flowering locus T or Ap3
 PT homolog activity, useful for immunological screening of cDNA expression
 PT libraries.
 PT
 XX
 XX Claim 17; Page 80-81; 88pp; English.
 PS
 XX
 CC The present invention relates to novel floral developmental proteins,
 CC more specifically flowering locus T (FT) or APETALA3 (AP3) homologue
 CC proteins and polynucleotides encoding such proteins. Floral developmental
 CC polynucleotides are useful for transforming cells or for producing plants
 CC by transforming the plant cells with the polynucleotides and regenerating
 CC the plants from the transformed plant cells. Sequences of the invention
 CC are useful for immunological screening of cDNA expression libraries. They
 CC are also useful for creating transgenic plants. Polynucleotides of the
 CC invention are used as probes for genetically and physically mapping the
 CC genes that they are a part of and as markers for traits linked to those
 CC genes. AP3 homologues may be useful for engineering plant sterility or
 CC fertility, flower development and morphology. FT or FT11 homologues are
 CC useful for engineering flowering time, plant growth rate, inflorescence
 CC architecture, tissue culture morphology and rate of cell division to
 CC enhance transformation. The present sequence is soybean AP3 homologue
 CC protein
 CC
 XX SQ Sequence 227 AA;
 Query Match 50.7%; Score 616.5; DB 5; Length 227;
 Best Local Similarity 52.2%; Pred. NO. 1.9e-49;
 Matches 118; Conservative 41; Mismatches 60; Indels 7; Gaps 3;
 QY 1 MARGKTEIKLIENTNQVYTSKRNGIFPKKAEQELTVLCDAKVSILMLNTNKHHEYISP 60
 DB 1 MARGKTIQKRIENTNQVYTSKRNGIFPKKAEQELTVLCDAKVSILMLNTNKHHEYISP 60
 QY 61 TTTTSGMYDDYQKTMGIDLWRTHESMKTLMKLEINNKLRREIRORGLHDNLGLSPDE 120
 DB 61 STSTKQFFDQYQMTLGVDLWNSHYENQENLKKLEVNRLNKEIRQRMGDCNLGLNED 120
 QY 121 LASLDDMQSSLDALRQRKHVTKTQETTTKKKYNLEQRGNMLHGVFDQEAAGEDPQY 180
 DB 121 LKLEBEMDKAAKVKERKVIQITNQIDTQKKNFNEKEVNRLLH---DLDAKAEDPRF 177

RESULT 8
 AAB32552
 ID AAB32552 standard; protein; 233 AA.
 XX
 AC AAB32552;
 XX
 DT 25-JAN-2001 (first entry)
 XX
 DE Eucalyptus grandis transcription factor protein sequence #10.
 XX
 KW Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
 KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
 KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
 KW homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
 KW type 2 Cys2His2; CCAAT box element; MYB.
 XX
 OS Eucalyptus grandis.
 XX
 FN WO2000053724-A2.
 XX
 PD 14-SEP-2000.
 XX
 XX 09-MAR-2000; 2000WO-US006112.
 PF
 XX 11-MAR-1999; 99US-00266513.
 PR
 XX 18-AUG-1999; 99US-0149485P.
 XX
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 XX
 XX Wood M, McGrath A, Shenk MA, Glenn M;
 PI
 XX WPI; 2000-579369/54.
 DR
 XX New isolated polynucleotide encoding a plant transcription factor for
 PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
 PT having modified gene expression or modified activity of a polypeptide.
 XX
 XX Claim 8; Page 203; 747pp; English.
 XX
 CC The present invention relates to novel plant transcription factors from
 CC Eucalyptus grandis or Pinus radiata. The present sequence is one such
 CC transcription factor. The transcription factor may be used to produce a
 CC plant having modified gene expression such as a woody plant e.g. a
 CC eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or
 CC to modify the activity of a polypeptide in a plant. The transcription
 CC factors of the present invention are members from the following families
 CC of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic
 CC helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain
 CC zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2
 CC Cys2His2, CCAAT box elements and MYB

Query Match 48.1%; Score 585.5; DB 3; Length 233;
 Best Local Similarity 51.3%; Pred. No. 1.6e-46;
 Matches 118; Conservative 40; Mismatches 63; Indels 9; Gaps 4;
 QY 1 MARGKTEIKLIENTNQVYTSKRNGIFPKKAEQELTVLCDAKVSILMLNTNKHHEYISP 60
 DB 1 MARGKTIQKRIENTNQVYTSKRNGIFPKKAEQELTVLCDAKVSILMLNTNKHHEYISP 60
 QY 61 TTTTSGMYDDYQKTMGIDLWRTHESMKTLMKLEINNKLRREIRORGLHDNLGLSPDE 120
 DB 61 STSTKQFFDQYQMTLGVDLWNSHYENQENLKKLEVNRLNKEIRQRMGDCNLGLNED 120
 QY 121 LASLDDMQSSLDALRQRKHVTKTQETTTKKKYNLEQRGNMLHGVFDQEAAGEDP 178

Db 121 LCGLEQMDNAVSLIBRKVKTLGNQIDTARKKKNAEINKSLQDWTNLIKHLREDDP 180
Qy 179 QYVENEDEGYSALASN--GANNLYTPHLH--HPNHLHGSSSLGSSIT 224
Db 181 HFGWVNGRDEYAVIGYTDAAARLYTLRLQDPQNLTSGG--GSEIT 227

RESULT 9
AAG25577
ID AAG25577 standard; protein; 232 AA.
XX AC AAG25577;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 29698.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
XX PR 09-MAR-1999; 99US-0123548P.
XX PR 23-MAR-1999; 99US-0125788P.
XX PR 25-MAR-1999; 99US-0126264P.
XX PR 29-MAR-1999; 99US-0126785P.
XX PR 01-APR-1999; 99US-0127462P.
XX PR 05-APR-1999; 99US-0128234P.
XX PR 08-APR-1999; 99US-0128714P.
XX PR 16-APR-1999; 99US-0129845P.
XX PR 19-APR-1999; 99US-0130077P.
XX PR 21-APR-1999; 99US-0130449P.
XX PR 23-APR-1999; 99US-0130510P.
XX PR 28-APR-1999; 99US-0131449P.
XX PR 30-APR-1999; 99US-0132048P.
XX PR 04-MAY-1999; 99US-0132407P.
XX PR 05-MAY-1999; 99US-0132484P.
XX PR 06-MAY-1999; 99US-0132486P.
XX PR 07-MAY-1999; 99US-0132487P.
XX PR 11-MAY-1999; 99US-0132863P.
XX PR 14-MAY-1999; 99US-0134218P.
XX PR 14-MAY-1999; 99US-0134219P.
XX PR 14-MAY-1999; 99US-0134221P.
XX PR 18-MAY-1999; 99US-0134370P.
XX PR 18-MAY-1999; 99US-0134768P.
XX PR 18-MAY-1999; 99US-0134941P.
XX PR 20-MAY-1999; 99US-0135124P.
XX PR 21-MAY-1999; 99US-0135353P.
XX PR 24-MAY-1999; 99US-0135629P.
XX PR 25-MAY-1999; 99US-0136021P.
XX PR 27-MAY-1999; 99US-0136392P.
XX PR 28-MAY-1999; 99US-0136782P.
XX PR 01-JUN-1999; 99US-0137222P.
XX PR 03-JUN-1999; 99US-0137528P.
XX PR 04-JUN-1999; 99US-0137502P.
XX PR 07-JUN-1999; 99US-0137724P.
XX PR 08-JUN-1999; 99US-0138094P.
XX PR 10-JUN-1999; 99US-0138540P.
XX PR 10-JUN-1999; 99US-0138847P.
XX PR 14-JUN-1999; 99US-0139119P.
XX PR 16-JUN-1999; 99US-0139452P.
XX PR 16-JUN-1999; 99US-0139453P.
XX PR 17-JUN-1999; 99US-0139492P.
XX PR 18-JUN-1999; 99US-0139454P.
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XX PR 18-JUN-1999; 99US-0139457P.
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XX PR 18-JUN-1999; 99US-0139461P.
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XX PR 18-JUN-1999; 99US-0139750P.
XX PR 18-JUN-1999; 99US-0139763P.
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XX PR 22-JUN-1999; 99US-0139899P.
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XX PR 23-JUN-1999; 99US-0140364P.
XX PR 24-JUN-1999; 99US-0140655P.
XX PR 28-JUN-1999; 99US-0140823P.
XX PR 29-JUN-1999; 99US-0140991P.
XX PR 30-JUN-1999; 99US-0141287P.
XX PR 01-JUL-1999; 99US-0141842P.
XX PR 01-JUL-1999; 99US-0142154P.
XX PR 02-JUL-1999; 99US-0142055P.
XX PR 06-JUL-1999; 99US-0142390P.
XX PR 08-JUL-1999; 99US-0142803P.
XX PR 09-JUL-1999; 99US-0142920P.
XX PR 12-JUL-1999; 99US-0142977P.
XX PR 13-JUL-1999; 99US-0143542P.
XX PR 14-JUL-1999; 99US-0143624P.
XX PR 15-JUL-1999; 99US-0144005P.
XX PR 16-JUL-1999; 99US-0144085P.
XX PR 16-JUL-1999; 99US-0144086P.
XX PR 19-JUL-1999; 99US-0144335P.
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XX PR 19-JUL-1999; 99US-0144335P.
XX PR 20-JUL-1999; 99US-0144352P.
XX PR 20-JUL-1999; 99US-0144632P.
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XX PR 10-AUG-1999; 99US-0148171P.
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XX PR 12-AUG-1999; 99US-0148341P.

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PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
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PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
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PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
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PR 28-SEP-1999; 99US-0156458P.
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PR 21-OCT-1999; 99US-0160767P.
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PR 21-OCT-1999; 99US-0160815P.
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PR 22-OCT-1999; 99US-0160989P.
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PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 46.8%; Score 569; DB 3; Length 222;
Best Local Similarity 53.3%; Pred. No. 5; Se-45;
Matches 114; Conservative 30; Mismatches 66; Indels 4; Gaps 2;

QY 1 MARGKLEITLLENQNRQVYSGRRNGIFPKAQOELTVLCDAVSLIMLSNTRKQHEIYSP 60
DB 1 MARGKQIRIENQNRQVYSGRRNGIFPKAQHEITVLCDAVSLIMSSSKQHEIYSP 60
QY 61 TTTTSMYDXYKTNGIDIMRTTHESMCDTLMKLEINNKLREIRQRGLGHDLNGLSPDE 120

DB 61 NNTTKEIYDVLYQITSDVWATQYERMQETKRKLLETNRNLRFTQIKRLGECINLDIOE 120
QY 121 LSLDDDEMSSLDALRQRKYHIKQTETTKKKVKNLEGRGNMHLGYPDOEAGEDPOY 180
DB 121 LRLEDEMENTFKLVREKFKSLGNQIETTKKNSQQDIQNLH---ELELRADENHY 177
QY 181 GYEDNEGDEYSALALSNGANMLYTFHLRPNLH 214
DB 178 GLVNGGDYDVLGYQIEGSRAYALRFHQ-NHHH 210

RESULT 10
AAG25576
ID AAG25576 standard; protein; 242 AA.
XX

AC AAG25576;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 29697.

XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

XX Arabidopsis thaliana.

OS EP1033405-A2.

XX 06-SEP-2000.

PD 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 09-MAR-1999; 99US-0123180P.

XX 22-MAR-1999; 99US-0125788P.

XX 29-MAR-1999; 99US-0126264P.

XX 01-APR-1999; 99US-0127462P.

XX 06-APR-1999; 99US-0128234P.

XX 16-APR-1999; 99US-0128714P.

XX 21-APR-1999; 99US-0130077P.

XX 23-APR-1999; 99US-0130510P.

XX 28-APR-1999; 99US-0131449P.

XX 30-APR-1999; 99US-0132048P.

XX 04-MAY-1999; 99US-0132407P.

XX 05-MAY-1999; 99US-0132485P.

XX 06-MAY-1999; 99US-0132486P.

XX 07-MAY-1999; 99US-0132863P.

XX 11-MAY-1999; 99US-0134218P.

XX 14-MAY-1999; 99US-0134219P.

XX 14-MAY-1999; 99US-0134221P.

XX 18-MAY-1999; 99US-0134370P.

PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135639P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.

QY 1 MARGKIEIKLIENTNQVTVYSKRRNGIPFKKAOELTVLCDAKSLIMLSNTNKGHEVISP 60
Db 11 MARGKIDIKRIENNTQVTVYSKRRNGIPFKKAOELTVLCDAKSLIMLSNTNKGHEVISP 70
QY 61 TTTTSTADYQKTMGDDIWRTHESKMDLMLKEINNTKREIRORLGHDLNGLSFDE 120
Db 71 NTTKKEIVDLVOTISDVWATQYERMOETKRLLETNRMLRTQIKQRLGECINKLDIOE 130
QY 121 LASIDDEMOSSLDAIPQRKYHVIKTQETETTKKYKNLEFORGNMLHGYPDOEAAGEDPOY 180
Db 131 LRRLEDEMENTFKLVREKFKSLGNQIETTKKKYKSQODIQKLIH---ELELRADPHY 187
QY 181 GYEDNEGYSALALNSGANNLYTFHLLHPYLLH 214
Db 188 GLVINGGDYDVLGVOLEGSPAYALRPHQ-NHHH 220

RESULT 11

AGS4023
ID AGS4029 standard; protein; 232 AA.

XX AC AAG54029;

XX DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 68844.

KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
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PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.

PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
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PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
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PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143824P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
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PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144632P.
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PR 21-JUL-1999; 99US-0145086P.
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PR 21-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 22-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
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PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.

Query Match 52.4%; Score 564; DB 3; Length 232;
Best Local Similarity 52.8%; Pred. No. 1, Ee-44;
Matches 113; Conservative 31; Mismatches 66; Indels 4; Gaps 2;

XX XX
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123568P.
PR 23-MAR-1999; 99US-0125788P.
PR 23-MAR-1999; 99US-0126284P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129645P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
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PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134570P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.

XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123568P.
PR 23-MAR-1999; 99US-0125788P.
PR 23-MAR-1999; 99US-0126284P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129645P.
PR 19-APR-1999; 99US-0130077P.
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PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
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PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
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PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134570P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.

AC AAG54679;
AC AAG54679;
AC AAG54679 standard; protein; 236 AA.
ID AAG54679
ID AAG54679
ID AAG54679 standard; protein; 236 AA.
XX AC AAG54679;
XX AC AAG54679;
XX DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 69759.
XX DE
XX DE
XX KM Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
XX KM
XX KM
XX OS Arabidopsis thaliana.
XX OS
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123568P.
PR 23-MAR-1999; 99US-0125788P.
PR 23-MAR-1999; 99US-0126284P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129645P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134570P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.

Dy 1 MARKEIKLIENTNQVYTKRRNGIFPKADELTVLCDAKVSILMLSTNKKHEYSIP 60
Db 1 MARKEIKLIENTNQVYTKRRNGIFPKAHELTVLCDAKVSIIIMFSSNNKLHEYISP 60
Qy 61 TTTTTSKYDDPOKTMGDIWRTHESMKDITLMKLEINNTLRREIRORIGHDINGLSFDE 120
Db 61 NTTTKEIVDLXQTISDVDMATQYERKOEETKRKILLETRNLRFQIKORLGECLDELIOE 120
Qy 121 LASIDDEMOSSLAIRQRKVHVIKTQETTTRKKVKVNLQRRGNMHLGYFDQEAAGEDPOY 180
Db 121 LRRLEDDEMENTFKLYVRERKFESLGNOIETTRKKKNKSQODIQKULIH--ELELRADPPHY 177
Qy 181 GYEDNEGDESALASNGANNVTFLHHHPNLH 214
Db 178 GLVDNGSDYDSVLGYQLSGRAYALRPHQ-NHHH 210

RESULT 12
AAG54679
AAG54679 standard; protein; 236 AA.

PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136352P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 14-JUN-1999; 99US-0138847P.
PR 16-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
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PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139889P.
PR 23-JUN-1999; 99US-0140353P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 30-JUN-1999; 99US-0140991P.
PR 01-JUL-1999; 99US-0141842P.
PR 02-JUL-1999; 99US-0142154P.
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PR 08-JUL-1999; 99US-0142390P.
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PR 23-JUL-1999; 99US-0145224P.
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PR 02-AUG-1999; 99US-0146386P.
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PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148665P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
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PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 01-SEP-1999; 99US-0151438P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
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PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157717P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 13-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
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PR 14-OCT-1999; 99US-0159638P.
PR 14-OCT-1999; 99US-0159684P.
PR 18-OCT-1999; 99US-0160741P.
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PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
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PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161559P.
PR 26-OCT-1999; 99US-0161360P.

PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 46.4%; Score 564; DB 3; Length 236;
Best Local Similarity 52.8%; Pred. No. 1,7e+44;
Matches 113; Conservative 31; Mismatches 66; Indels 4; Gaps 2;

QY 1 MARGKIKIKLENTNQTNRQVYSSKRRNGIFPKACQELTYLDCAKYSLNLSNTNQCHEYISF 60
DB 5 MARGKIKIKLENTNQTNRQVYSSKRRNGIFPKACQELTYLDCAKYSLNLSNTNQCHEYISF 64
QY 61 TTTTTSKYDYQKTMGIDLWRTHEESKMDLWKLKKEINNKLRERIQRLCHDINGLSFDE 120
DB 65 NTTTKEIVDYQITISDVAVATQYERMOETKRLLETNRNLRQIQRLCECDKLDIOE 124
QY 121 LASLIDEMOSSLDAIFORKYHVIKTQETETTKKKYKNLEGRGMHLGYFPOEAAAGDPDY 160
DB 125 LRRLEDEMENTFKLVKRRKFKSLGNQLETTKKKKKSOODIQKNLH---ELELRADPHY 181
QY 181 GYEDNEGDEYASALALNSGANNLYTFHLHPNLMH 214
DB 182 GLVDMGSDYDVLGYQIEGSRAYALRPHQ-NHHH 214

RESULT 13

AA654028 standard; protein; 241 AA.

AA654028;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 68843.

KW Protein identification; signal transduction pathway; metabolic pathway;
XM hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

XX Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
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PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.
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PR 14-MAY-1999; 99US-0134370P.
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PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
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PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 16-JUN-1999; 99US-0139119P.
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PR 18-JUN-1999; 99US-0139454P.
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PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
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PR 26-JUL-1999; 99US-0145276P.
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 PR 27-JUL-1999; 99US-0145919P.
 PR 28-JUL-1999; 99US-0145921P.
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 PR 05-AUG-1999; 99US-0147192P.
 PR 05-AUG-1999; 99US-0147260P.
 PR 06-AUG-1999; 99US-0147303P.
 PR 06-AUG-1999; 99US-0147416P.
 PR 09-AUG-1999; 99US-0147935P.
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 PR 16-AUG-1999; 99US-0149368P.
 PR 17-AUG-1999; 99US-0149175P.
 PR 18-AUG-1999; 99US-0149426P.
 PR 20-AUG-1999; 99US-0149722P.
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 PR 23-AUG-1999; 99US-0149902P.
 PR 23-AUG-1999; 99US-0149930P.
 PR 25-AUG-1999; 99US-0150565P.
 PR 26-AUG-1999; 99US-0150884P.
 PR 27-AUG-1999; 99US-0151065P.
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 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-0155659P.
 PR 29-SEP-1999; 99US-0156458P.
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 PR 07-OCT-1999; 99US-0158022P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
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 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
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 PR 22-OCT-1999; 99US-0160989P.

PR 25-OCT-1999; 99US-0161404P.
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 PR 25-OCT-1999; 99US-0161406P.
 PR 25-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 26-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161933P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 46.4%; Score 564; DB 3; Length 241;
 Best Local Similarity 52.8%; Pred. No. 1,7e-44;
 Matches 113; Conservative 31; Mismatches 66; Indels 4; Gaps 2;

QY 1 MARGKIEIKLIEQNTROYTSGRRNGIFPKAQELTVLCDAYSLIMLSNTNMHEVISP 60
 DB 10 MARGKIQIKRIENQTRQYTSKRNGLPKQKHELTVLCDAYSLIMSSSKHETVISP 69
 QY 61 TTTTSMYDDYQKTMGIDIMRTHEBSKQDLMKLEINNKLRREIRQRLGHDINGLSFDE 120
 DB 70 NTTTKEIVDLQYTSIDVDVWATQYERMQETKRLLETNNRLTQIKQRLGECIDEDHIOE 129
 QY 121 LASIDEMOSSLDATQQRKHYIKTQTEFTKKKKVNLBGRBNMLGYPDQAGDPDY 180
 DB 130 LRRLEDEMENTFELVVERKPKSLGNQIFTKKKNSQDIOQLNLH--ELERADDPHY 186
 QY 181 GYEDNEGDEYSALALNSGANNLYTFRLHHPNLH 214
 DB 187 GLVDNGGDYDVLGVQIEGSRVALRFHQ-NHHH 219

RESULT 14
 AAE25755
 ID AAE25755 standard; protein; 227 AA.
 XX
 AC AAE25755;
 XX
 DT 04-NOV-2002 (first entry)
 XX
 DE Corn AP3 homologue protein from clone ctain.pk0050.f8.
 XX
 KW Floral developmental protein; flowering locus T; APTAL3; transgenic;
 KW FT; AP3; transgenic plant; fertility; flower development; gene mapping;
 KW fertility; plant growth; inflorescence architecture; plant morphology;
 KW tissue culture; cell division; corn.
 XX
 OS Zea mays.
 XX
 PN WC0200244390-A2.
 XX
 PD 06-JUN-2002.
 XX
 PE 21-NOV-2001; 2001WO-US043750.
 XX
 PR 28-NOV-2000; 2000US-0253415P.
 XX
 PA (DUPO) DU POINT DE NEMOURS & CO E I.
 XX
 XT Cahoon EB, Cahoon RE, Klein TW, Rafalski AJ, Sakai H;
 XX
 XX WPI; 2002-547703/58.
 DR N-PADB; AAD42257.
 XX
 PT New floral developmental polypeptide having flowering locus T or Ap3
 PT homology activity, useful for immunological screening of cDNA expression
 FT libraries.
 XX
 PS Claim 18; Page 78; 88pp; English.
 XX
 CC The present invention relates to novel floral developmental proteins,
 CC more specifically flowering locus T (FT) or APTAL3 (AP3) homologue
 CC proteins and polynucleotides encoding such proteins. Floral developmental

CC polynucleotides are useful for transforming cells or for producing plants
CC by transforming the plant cells with the polynucleotides and regenerating
CC the plants from the transformed plant cells. Sequences of the invention
CC are useful for immunological screening of cDNA expression libraries. They
CC are also useful for creating transgenic plants. Polynucleotides of the
CC invention are used as probes for genetically and physically mapping the
CC genes that they are a part of and as markers for traits linked to those
CC genes. AP3 homologues may be useful for engineering plant sterility or
CC fertility, flower development and morphology. FT or FTL homologues are
CC useful for engineering flowering time, plant growth rate, inflorescence
CC architecture, tissue culture morphology and rate of cell division to
CC enhance transformation. The present sequence is corn AP3 homologue
CC protein.

XX SQ Sequence 227 AA;

Query Match 45.5%; Score 553.5; DB 5; Length 227;
Best Local Similarity 51.0%; Pred. No. 1.5e-43;
Matches 122; Conservative 33; Mismatches 63; Indels 21; Gaps 7;

QY 1 MARGKIEIKLIENQTNROVYTSKRNRGIFPKAQLTVLCDAKVSLMLSTNKGHEVISP 60
DB 1 MGRKIEIKRIENATNRQVYTSKRRTGIMKKARELVLCDAQVALIMFSSTGKYHEFCSP 60

QY 61 TTTTSMYDDYQKTMGIDLWRTHEESKDTLMKLEINNKLRREIRORLGHDLNGLSFDE 120
DB 61 GTDIKTFDRYQQAIGTSLWIEQYENMQRTLSHLKQINRGIRFEIRQMGEDLDLSDFDE 120

QY 121 LASIDDEMOSLDAIRORXHYVKTQETETTKKKVKYKLEQRGMMLHGFDQBAAG--EPP 178
DB 121 LRGLQNVDAALKEVRHRKXHVITQETETTKKKVKYKLEQRGMMLHGFDQBAAG--EPP 174

QY 179 QYGYEDNEG--DYESALALSNGA--NNLYTFHL--HHPNLHGGSSLGSSITLHDLRL 231
DB 175 AFGVNTGAGVAMDGAALGAPDPAFRRVPSQPNLH--GMYAG--FHLRL 226

RESULT 15

AAE25763 ID AAE25763 standard; protein; 224 AA.

XX AC AAE25763;

XX DT 04-NOV-2002 (first entry)

XX DE Rice MADS box-like protein.

XX KM Floral developmental protein; flowering locus T; APETALA3; transgenic;

XX KM FT; AP3; transgenic plant; fertility; flower development; gene mapping;

XX KM sterility; plant growth; inflorescence architecture; plant morphology;

XX KM tissue culture; cell division; rice; MADS box-like protein.

XX OS Oryza sativa.

XX PN WO200244390-A2.

XX PD 06-JUN-2002.

XX PE 21-NOV-2001; 2001WO-US043750.

XX PR 28-NOV-2000; 2000US-0253415P.

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX PI Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;

XX DR WPI; 2002-547703/58.

XX PT New floral developmental polypeptide having flowering locus T or AP3
XX PT homolog activity, useful for immunological screening of cDNA expression
XX PT libraries.

PS Example 4; Page 82-83; 88pp; English.

XX The present invention relates to novel floral developmental proteins,
CC more specifically flowering locus T (FT) or APETALA3 (AP3) homologue
CC proteins and polynucleotides encoding such proteins. Floral developmental
CC polynucleotides are useful for transforming cells or for producing plants
CC by transforming the plant cells with the polynucleotides and regenerating
CC the plants from the transformed plant cells. Sequences of the invention
CC are useful for immunological screening of cDNA expression libraries. They
CC are also useful for creating transgenic plants. Polynucleotides of the
CC invention are used as probes for genetically and physically mapping the
CC genes that they are a part of and as markers for traits linked to those
CC genes. AP3 homologues may be useful for engineering plant sterility or
CC fertility, flower development and morphology. FT or FTL homologues are
CC useful for engineering flowering time, plant growth rate, inflorescence
CC architecture, tissue culture morphology and rate of cell division to
CC enhance transformation. The present sequence is rice MADS box-like
CC protein. This sequence is used in the exemplification of the invention
CC protein.

XX SQ Sequence 224 AA;

Query Match 45.1%; Score 548; DB 5; Length 224;
Best Local Similarity 50.2%; Pred. No. 4.9e-43;
Matches 120; Conservative 31; Mismatches 64; Indels 24; Gaps 6;

QY 1 MARGKIEIKLIENQTNROVYTSKRNRGIFPKAQLTVLCDAKVSLMLSTNKGHEVISP 60
DB 1 MGRKIEIKRIENATNRQVYTSKRRTGIMKKARELVLCDAQVALIMFSSTGKYHEFCSP 60

QY 61 TTTTSMYDDYQKTMGIDLWRTHEESKDTLMKLEINNKLRREIRORLGHDLNGLSFDE 120
DB 61 STDKIGIFDRYQQAIGTSLWIEQYENMQRTLSHLKQINRGIRFEIRQMGEDLDLSDFDE 120

QY 121 LASIDDEMOSLDAIRORXHYVKTQETETTKKKVKYKLEQRGMMLHGFDQBAAG--EPP 174
DB 121 LRGLQNVDAALKEVRHRKXHVITQETETTKKKVKYKLEQRGMMLHGFDQBAAG--EPP 170

QY 175 QYGYEDNEGDIYBSALALSNGANLYTFHL--HHPNLHGGSSLGSSITLHDLRL 231
DB 171 REEPAFGVNTGGWGDGAGAAADMAFRRVPSQPNLH--GMYAGN--HDLRL 223

Search completed: September 27, 2004, 09:25:12
Job time : 93.3848 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 09:28:25 ; Search time 89.7897 Seconds
(without alignments)
830.848 Million cell updates/sec

Title: US-10-069-527-4

Perfect score: 1216
Sequence: 1 MARGKEIKIENOTNRQVT.....HGGSSLGSSITLHDLRLA 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1349238 seqs, 321558718 residues

Total number of hits satisfying chosen parameters: 1349238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	709.5	58.3	227	14	US-10-104-580-4
2	655.5	53.9	241	12	US-10-425-114-44825
3	652	53.6	260	12	US-10-425-114-39286
4	640.5	52.7	261	12	US-10-425-114-46248
5	631.5	51.9	243	12	US-10-424-599-209491
6	604.5	49.7	227	12	US-10-424-599-263636
7	576.5	47.4	223	12	US-10-425-114-42492
8	557	45.8	234	12	US-10-424-599-263637
9	474	39.0	143	12	US-10-425-114-41663
10	398	32.7	186	16	US-10-437-963-132081
11	383	31.5	208	12	US-10-424-599-208168
12	383	31.5	209	12	US-10-425-114-40799
13	373.5	30.7	207	12	US-10-424-599-175060
14	368.5	30.3	205	12	US-10-425-114-39944
15	331.5	27.3	208	12	US-10-412-699B-56

16	310	25.5	235	16	US-10-437-963-120366	Sequence 120366,
17	310	25.5	260	16	US-10-437-963-113197	Sequence 113197,
18	305.5	25.1	240	9	US-09-970-624-2	Sequence 2, Appl1
19	301	24.8	228	12	US-10-425-114-66169	Sequence 66169, A
20	301	24.8	289	16	US-10-437-963-173987	Sequence 173987,
21	297	24.4	189	16	US-10-437-963-153788	Sequence 153788,
22	296.5	24.4	221	12	US-10-412-699B-1728	Sequence 1728, Ap
23	295.5	24.3	249	12	US-10-425-114-54913	Sequence 54913, A
24	295.5	24.3	249	12	US-10-425-114-56968	Sequence 56968, A
25	295.5	24.3	249	12	US-10-425-114-61531	Sequence 61531, A
26	295.5	24.3	249	12	US-10-425-114-72229	Sequence 72229, A
27	295.5	24.3	288	12	US-10-425-114-42198	Sequence 42198, A
28	295.5	24.3	298	12	US-10-425-114-42117	Sequence 42117, A
29	291	23.9	233	12	US-10-425-114-38851	Sequence 38851, A
30	290.5	23.9	238	10	US-09-934-455-8	Sequence 8, Appl1
31	290.5	23.9	238	12	US-10-412-699B-68	Sequence 68, Appl
32	290.5	23.9	238	12	US-10-225-066A-328	Sequence 328, App
33	290.5	23.9	238	14	US-10-285-264-34	Sequence 34, Appl
34	290.5	23.9	238	15	US-10-374-780A-14	Sequence 14, Appl
35	290.5	23.9	282	12	US-10-424-599-156275	Sequence 156275,
36	288.5	23.7	228	10	US-09-819-142-4	Sequence 4, Appl1
37	288.5	23.7	228	10	US-09-934-455-32	Sequence 32, Appl
38	288.5	23.7	228	12	US-10-412-699B-938	Sequence 938, App
39	287	23.6	241	12	US-10-425-114-67499	Sequence 67499, A
40	287	23.6	247	12	US-10-425-114-40879	Sequence 40879, A
41	287	23.6	283	12	US-10-425-114-56978	Sequence 56978, A
42	287	23.6	283	12	US-10-425-114-56979	Sequence 56979, A
43	287	23.6	283	12	US-10-425-114-56989	Sequence 56989, A
44	287	23.6	292	12	US-10-425-114-39538	Sequence 39538, A
45	286.5	23.6	245	12	US-10-424-599-201348	Sequence 201348,

ALIGNMENTS

RESULT 1
US-10-104-580-4
; Sequence 4, Application US/10104580
; Publication No. US20030033628A1
GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 62486
; CURRENT APPLICATION NUMBER: US/10/104,580
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 09/410,464
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/287,700
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,851
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 4
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Populus balsamifera subsp. trichocarpa
US-10-104-580-4
Query Match 58.3%; Score 709.5; DB 14; Length 227;
Best Local Similarity 62.3%; Pred. No. 9.1e-59;
Matches 149; Conservativity 24; Mismatches 45; Indels 21; Gaps 5;
Cy 1 MARGKEIKIENOTNRQVTYSKRNGIFKXQELTVLCLDAKVSILMTSNTKMEHYISP 60
Db 1 MARGKEIKIENPTNRQVTYSFRNGIFKXQELTVLCLDAKVSILMTSNTKMEHYISP 60
Cy TTTTSMYDDYQKTMGIDLRTHESMKTLMKKEINKKREIFORGHDLNGISFPE 120
Db TTTTSMYDDYQKTMGIDLRTHESMKTLMKKEINKKREIFORGHDLNGISFPE 120
Cy STTKKIYQYQNALGIDMGQYEMQKHLKNDINKLQELRQREGGINDLSIH 120
Db STTKKIYQYQNALGIDMGQYEMQKHLKNDINKLQELRQREGGINDLSIH 120
Cy 121 LASIDEMQSLDAIRQKRVHVKIQTETTKKKVKLQQRGNMLHGYDQBAAGSDPY 180
Db 121 LASIDEMQSLDAIRQKRVHVKIQTETTKKKVKLQQRGNMLHGYDQBAAGSDPY 180

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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3049-050-F6_FLI.pep
US-10-425-114-39286

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RESULT 2

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US-10-425-114-44825
; Sequence 44825, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 44825
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701209467_FLI.pep
US-10-425-114-44825

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Query Match      53.9%; Score 655.5; DB 12; Length 241;
Best Local Similarity 59.2%; Pred. No. 1.3e-53;
Matches 142; Conservative 32; Mismatches 51; Indels 15; Gaps 7;

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QY 1 MARGKIKIKLENTNQVYTSKRNGIFPKAQLTYLCAKXSLMTSLNTNKGHEYISP 60
DB 9 MGRGKIKIKLENTNQVYTSKRNGIFPKAQLTYLCAKXSLMTSLNTNKGHEYISP 68
QY 61 TTTTSMYDDYQKTMG-IDLWRTHEESKMDLWKLKEINNKLRREIRQRIQH--DLNGLS 117
DB 69 GLTTKRIIDYQKTLGIDILWHSHEYKMLENKKLIDINNKLRQIRHRIGEGLDMDMS 128
QY 118 FDELASLDDDEMOSLDAIRQKXHVITQETETTKKKYKNEQRRGNMLHGYFPOEAAAGD 177
DB 129 FQQLRTLEEDWVSSIGIKRERKRFVITKRTDTCRKVKSLQKNNRDL--FELECAIH 185
QY 178 PÖGYEDNEGDYESALALSGANNLYTF-HLHHPNL---HHGSSISGSSITHDLRLA 232
DB 186 PÖFILHD-EGDEESAVVALANGASTLVAFCHQHSHSLNLPESH---SHGEPPFTDIDLRLA 241

```

RESULT 3

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US-10-425-114-39286
; Sequence 39286, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 39286
; LENGTH: 260

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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3049-050-F6_FLI.pep
US-10-425-114-39286

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Query Match      53.6%; Score 652; DB 12; Length 260;
Best Local Similarity 57.9%; Pred. No. 3e-53;
Matches 143; Conservative 31; Mismatches 53; Indels 20; Gaps 8;

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QY 1 MARGKIKIKLENTNQVYTSKRNGIFPKAQLTYLCAKXSLMTSLNTNKGHEYISP 60
DB 19 MGRGKIKIKLENTNQVYTSKRNGIFPKAQLTYLCAKXSLMTSLNTNKGHEYISP 78
QY 61 TTTTSMYDDYQKTMG-IDLWRTHEESKMDLWKLKEINNKLRREIRQRIQH--DLNGLS 117
DB 79 GLTTKRIIDYQKTLGIDILWHSHEYKMLENKKLIDINNKLRQIRHRIGEGLDMDMS 138
QY 118 FDELASLDDDEMOSLDAIRQKXHVITQETETTKKKYKNEQRRGNMLHGYFPOEAAAGD 177
DB 139 FQQLRTLEEDWVSSIGIKRERKRFVITKRTDTCRKVKSLQKNNRDL--FELECAIH 195
QY 178 PÖGYEDNEGDYES-----ALALSGANNLYTF-HLHHPNL---HHGSSISGSSITH 225
DB 196 PÖFILHD-EGDEESAAAAAVALANGASTLVAFCHQHSHSLNLPESHNGEPPFTDIDLRLA 254
QY 226 LHDRLA 232
DB 255 -HDLRLA 260

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RESULT 4

```

US-10-425-114-46248
; Sequence 46248, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46248
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701148021_FLI.pep
US-10-425-114-46248

```

```

Query Match      52.7%; Score 640.5; DB 12; Length 261;
Best Local Similarity 57.5%; Pred. No. 3.7e-52;
Matches 142; Conservative 31; Mismatches 55; Indels 19; Gaps 8;

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QY 1 MARGKIKIKLENTNQVYTSKRNGIFPKAQLTYLCAKXSLMTSLNTNKGHEYISP 60
DB 19 MGRGKIKIKLENTNQVYTSKRNGIFPKAQLTYLCAKXSLMTSLNTNKGHEYISP 78
QY 61 TTTTSMYDDYQKTMG-IDLWRTHEESKMDLWKLKEINNKLRREIRQRIQH--DLNGLS 117
DB 79 GLTTKRIIDYQKTLGIDILWHSHEYKMLENKKLIDINNKLRQIRHRIGEGLDMDMS 138
QY 118 FDELASLDDDEMOSLDAIRQKXHVITQETETTKKKYKNEQRRGNMLHGYFPOEAAAGD 177
DB 139 FQQLRTLEEDWVSSIGIKRERKRFVITKRTDTCRKVKSLQKNNRDL--FELECAIH 196
QY 178 PÖGYEDNEGDYES-----ALALSGANNLYTF-HLHHPNL---HHGSSISGSSITH 225

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Page 3

Query Match	47.4%	Score 576.5	DB 12	Length 223
Best Local Similarity	50.5%	Pred. No. 3,36-46		
Matches 112	Conservative 40	Mismatches 63	Indels 7	Gaps 3

QY	5	KIEIKLIENTONTQVYTSKRRNGIFPKAQLTVLCDKAVSLIMLSNTNKKHHEYISPTTTT	64
Db	1	KIQIRIENTNTNQVTSKRRNGIFPKANSLTVLCDKAVSIIMSSGKHHEYISPTST	60
QY	65	KSNWDDYQKTMGLDLMWTHESMKDITLWKKEIINNKKRREIRQSLGHDLNGLSFDEALSL	124
Db	61	KQEPDQYQKTMGLDLMWTHSHYENNOENKKLKDVRNKRKEIRQSGCGLNDLGHEDLKL	120
QY	125	DDMOSSLDAIRQKRYHVIKTQETTKKKYKYNLEQRRGNLHGYPDEAAGDPQCYED	184
Db	121	EEENDKAKAVRRERKYVITNOIDTQCKKFNNEKEVINRILR---DIDARAEDEPRFALID	177
QY	185	NEGDEYSALALNSGANNLYTFHH--HPPNLHHGSSLSGSSIT	224
Db	178	NGEYESVITGFSNLGPRMFAALSLQPSRPSAQSGAA--GSDILT	217

RESULT 8
 US-10-424-599-263637
 ; Sequence 263637, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 263637
 ; LENGTH: 234
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURES:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_80084C.1.pcp
 US-10-424-599-263637

Query Match 45.8%; Score 557; DB 12; Length 234;
 Best Local Similarity 48.1%; Pred. No. 2.5e-44;
 Matches 112; Conservative 41; Mismatches 66; Indels 14; Gaps 4;

QY 1 MARGKIEIKLENOTNROVYTSKRNGIFKKAQELTVLCAKYSILMLSTNKHETISP 60
 DB 1 MARGKIEIKLENOTNROVYTSKRNGIFKKAQELTVLCAKYSILMLSTNKHETISP 60
 QY 61 TTTKSMYDDYQKTMGIDLMRTHEESMKDLMKLEINNKLRREIRQRLGHDNGLSPDE 120
 DB 61 STSKQFPDQYQMTLGVDLWNSHYENMQENLKKLKVNRRLRKEIRQMGDCINDLGMED 120
 QY 121 LASIDDEMOSSLDAIRQK-----KXHVIKTQETTTKKVKVRLQGRGNMLHGYDQA 173
 DB 121 LKLEEMDMKAAKAVRRKSCMTWREKQKHTHRIIVQRKKFNNEKVENHRLR---DIDA 177
 QY 174 AGEDPQYEDNEBGYESALALNSGANNLYTFPHL--HPNLHHGSSSLGSSIT 224
 DB 178 RAEDPRRALIDNGEYEVSVIGFSLGPRMFLSLQSPHPSAQGAA--GSDLT 228

RESULT 9
 US-10-425-114-41663
 ; Sequence 41663, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 41663
 ; LENGTH: 143
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURES:
 ; OTHER INFORMATION: Clone ID: jC-gmf102220148g99_FLI.pcp
 US-10-425-114-41663

Query Match 39.0%; Score 474; DB 12; Length 143;
 Best Local Similarity 62.6%; Pred. No. 8.8e-37;
 Matches 87; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

QY 1 MARGKIEIKLENOTNROVYTSKRNGIFKKAQELTVLCAKYSILMLSTNKHETISP 60
 DB 4 MARGKIEIKLENOTNROVYTSKRNGIFKKAQELTVLCAKYSILMLSTNKHETISP 63
 QY 61 TTTKSMYDDYQKTMGIDLMRTHEESMKDLMKLEINNKLRREIRQRLGHDNGLSPDE 120
 DB 64 STSKQFPDQYQMTLGVDLWNSHYENMQENLKKLKVNRRLRKEIRQMGDCINDLGMED 123
 QY 121 LASIDDEMOSSLDAIRQK 139
 DB 124 LKLEEMDMKAAKAVRRK 142

RESULT 10
 US-10-437-963-132081
 ; Sequence 132081, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Batbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 132081
 ; LENGTH: 186
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURES:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_34084C.1.pcp
 US-10-437-963-132081

Query Match 32.7%; Score 398; DB 16; Length 186;
 Best Local Similarity 41.0%; Pred. No. 1.9e-29;
 Matches 98; Conservative 29; Mismatches 50; Indels 62; Gaps 9;

QY 1 MARGKIEIKLENOTNROVYTSKRNGIFKKAQELTVLCAKYSILMLSTNKHETISP 60
 DB 1 MARGKIEIKLENOTNROVYTSKRNGIFKKAQELTVLCAQVAIIMFSSTGNI----- 54
 QY 61 TTTKSMYDDYQKTMGIDLMRTHEESMKDLMKLEINNKLRREIRQRLGHDNGLSPDE 120
 DB 55 ---KGIIDRYQQAIGTSLMIB-----QRMEDLDGLEFDE 87
 QY 121 LASIDDEMOSSLDAIRQKXHVIKTQETTTKKVKVRLQGRGNMLHGY-----PDGE-AA 174
 DB 88 LRLEQNVDAAL-----XEVIVITQETETVKKVK-----HSYEAYETLQCELTGL 132
 QY 175 GEDPQYEDNEBGYESALALNSGANNLYTFHL--HPNLHHGSSSLGSSITLHDLRL 231
 DB 133 REEPAFGVNVTGGGMDGAGAGAAADMFAFRVVPSPQNLH--GMAYGN---HDLRL 185

RESULT 11
 US-10-424-599-208168
 ; Sequence 208168, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 208168
LENGTH: 208
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_2C.1.pep
US-10-424-599-208168

Query Match 31.5%; Score 383; DB 12; Length 208;
Best Local Similarity 38.8%; Pred. No. 5.8e-28;
Matches 83; Conservative 43; Mismatches 76; Indels 12; Gaps 3;

QY 1 MARGKIEIKLENTQNRQVTSKRRNGIFKKAQELTVLCAKVSLLMLSTNKKHEIYSP 60
DB 1 MGRGKIEIKRLENSNRQVTSKRRNGILKKAKEITVLCDAQVSLIFPAASGRKHDIYSP 60
QY 61 TTTKSMYDDYQKTWIGIDIMRTHESMKDTLWKLEINNKLRREIRQRLGHDINGLSFDE 120
DB 61 STTILIDILERYHKTSGKRLMDAKHENLNGEIERLKENDSQWIELRHLKGDIDINSINYKE 120
QY 121 LASTIDEMOSSLDALRQRKHVITKTQETTTKKKYNLEQRGNMLHGVPQEAAGEPQY 180
DB 121 LMALEDALJETGLVSRKQMDVYRMLR--NDKILBENRBLNPLMOQRLAEGAREVDN 178
QY 181 GYEDNEGDEYESALALSGANNLYTFHLH--HPNL 212
DB 179 GFDQSVRDYNSHMP-----FAFRVQPMQPNL 204
OTHER INFORMATION: Clone ID: PAT_MRT3847_129098C.1.pep
US-10-424-599-175060

RESULT 12
US-10-425-114-40799
Sequence 40799, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 40799
LENGTH: 209
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LIB3030-006-D8_FLI.pep
US-10-425-114-40799

Query Match 31.5%; Score 383; DB 12; Length 209;
Best Local Similarity 38.8%; Pred. No. 5.9e-28;
Matches 83; Conservative 43; Mismatches 76; Indels 12; Gaps 3;
QY 1 MARGKIEIKLENTQNRQVTSKRRNGIFKKAQELTVLCAKVSLLMLSTNKKHEIYSP 60
DB 2 MGRGKIEIKRLENSNRQVTSKRRNGILKKAKEITVLCDAQVSLIFPAASGRKHDIYSP 61
QY 61 TTTKSMYDDYQKTWIGIDIMRTHESMKDTLWKLEINNKLRREIRQRLGHDINGLSFDE 120
DB 61 STTILIDILERYHKTSGKRLMDAKHENLNGEIERLKENDSQWIELRHLKGDIDINSINYKE 121
QY 121 LASTIDEMOSSLDALRQRKHVITKTQETTTKKKYNLEQRGNMLHGVPQEAAGEPQY 180
DB 121 LMALEDALJETGLVSRKQMDVYRMLR--NDKILBENRBLNPLMOQRLAEGAREVDN 179

QY 181 GYEDNEGDEYESALALSGANNLYTFHLH--HPNL 212
DB 180 GFDQSVRDYNSHMP-----FAFRVQPMQPNL 205
OTHER INFORMATION: Clone ID: PAT_MRT3847_129098C.1.pep
US-10-424-599-175060

RESULT 13
US-10-424-599-175060
Sequence 175060, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovalic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 175060
LENGTH: 207
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(207)
OTHER INFORMATION: unsure at all xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_129098C.1.pep
US-10-424-599-175060

Query Match 30.7%; Score 373.5; DB 12; Length 207;
Best Local Similarity 37.7%; Pred. No. 4.6e-27;
Matches 81; Conservative 45; Mismatches 74; Indels 15; Gaps 3;
QY 1 MARGKIEIKLENTQNRQVTSKRRNGIFKKAQELTVLCAKVSLLMLSTNKKHEIYSP 60
DB 1 MGRGKIEIKRLENSNRQVTSKRRNGILKKAKEISVLCDAQVSLIFPAASGRKHDIYSP 60
QY 61 TTTKSMYDDYQKTWIGIDIMRTHESMKDTLWKLEINNKLRREIRQRLGHDINGLSFDE 120
DB 61 STTILIDILERYHKTSGKRLMDAKHENLNGEIERLKENDSQWIELRHLKGDIDINSINYKE 120
QY 121 LASTIDEMOSSLDALRQRKHVITKTQETTTKKKYNLEQRGNMLHGVPQEAAGEPQY 177
DB 121 LMALEDALJETGLVSRKQMDVYRMLR--NDKILBENRBLNPLMOQRLAEGAREVDN 176
QY 178 GYEDNEGDEYESALALSGANNLYTFHLHHPNL 212
DB 177 MONGFNEIKRVFNSHMQRAA-----LKQPNL 203

RESULT 14
US-10-425-114-39944
Sequence 39944, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 39944
LENGTH: 205
TYPE: PRT

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; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700903463_FLI pep
US-10-425-114-39944

Query Match          30.3%; Score 368.5; DB 12; Length 205;
Best Local Similarity 42.1%; Pred. No. 1.3e-26;
Matches 77; Conservative 37; Mismatches 48; Indels 21; Gaps 3;

QY 1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSLLMSTNKGHEIYSP 60
DB 25 MGRGKIEIKRIENSNNQVYTSKRNGILTKAKEISVLCDQVSLIFVSGKMGHEIYSP 84
QY 61 TTTTSMYDDYQKTMGIDLWRTHEESKQDLMKLEINNKLRREIRQRGLDNGLSFDE 120
DB 85 STTIDVLDYRQASGKTLMDAKHENLSNEIDRIKKENDSMQELHKLKGEDITSINYKE 144
QY 121 LASLDDMQSSLDARQKXHVITQTEYTKKKVKNLEGR-----GNN 164
DB 145 LMALEDLLENGLSGVREKKQVHR---MFKRNDKILLEGONKELNFLQOHLALBEGVGM 200
QY 165 LKG 167
DB 201 -HG 202

RESULT 15
US-10-412-699B-56
; Sequence 56; Application US/10412699B
; Publication No. US2004045049A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Zhang, James
; APPLICANT: Fromm, Michael E.
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Riethmann, Jose Luis
; APPLICANT: Adam, Luc J.
; APPLICANT: Broun, Pierre E.
; APPLICANT: Pineda, Omalra
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddie, James S.
; APPLICANT: Yu, Guo-liang
; APPLICANT: Uiang, Cai-Zhong
; APPLICANT: Samaha, Raymond R.
; APPLICANT: Pilgram, Marsha L.
; APPLICANT: Creelman, Robert A.
; APPLICANT: Dubell, Arnold N.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Kimimoto, Roderick
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI-0048CIP
; CURRENT APPLICATION NUMBER: US/10/412,699B
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 09/489,376
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: 09/506,720
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 09/533,030
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,648
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/819,142

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; PRIOR FILING DATE: 2001-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: Patent version 3.2
; SEQ ID NO 56
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G134
US-10-412-699B-56

Query Match          27.3%; Score 331.5; DB 12; Length 208;
Best Local Similarity 36.0%; Pred. No. 4.3e-23;
Matches 71; Conservative 39; Mismatches 64; Indels 23; Gaps 3;

QY 1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSLLMSTNKGHEIYSP 60
DB 1 MGRGKIEIKRIENANRVTFSSKRNGILYKAKEITVLCDQKVALIFASNGKMDYCCP 60
QY 61 TTTTSMYDDYQKTMGIDLWRTHEESKQDLMKLEINNKLRREIRQRGLDNGLSFDE 120
DB 61 SMDLGAMLDYQKLSGKTLMDAKHENLSNEIDRIKKENDSLQELHKLKGEDITSINYKE 120
QY 121 LASLDDMQSSLDARQKXHVITQTEYTKKKVKNLEGR-----RGNNL 165
DB 121 LMAVEHAIENGLDKVRHQWELLISKRRNEKMAEBGRQLTFQDQCEMAIASNAGVGM 180
QY 166 HGTFDQBAAGDPQYGY 182
DB 181 RDH-----DQGFQY 189

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Search completed: September 27, 2004, 09:44:50
Job time : 90.7897 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 09:19:49 / Search time 25.9508 Seconds
(without alignments)
859.952 Million cell updates/sec

Title: US-10-069-527-4
Perfect score: 1216
Sequence: 1 MARKIKIKIENQJNRQVT.....HGGSSISGSIHLHLRLA 232

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR.78:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	696.5	57.3	222	2 S23731	MADS box protein T
2	667.5	54.9	227	2 S12378	MADS box protein d
3	641.5	52.8	231	2 S31693	MADS box protein g
4	628.5	51.7	228	2 T07066	MADS box protein h
5	624.5	51.4	228	2 T07410	MADS box protein h
6	620.5	51.0	229	2 T09335	MADS-box protein h
7	564	46.4	232	2 A42095	floral homeotic pr
8	558.5	45.9	224	2 T14473	MADS box protein 2
9	549	45.1	214	2 T10715	MADS box protein c
10	544.5	44.8	224	2 T14474	MADS box protein c
11	500.5	41.2	203	2 T06277	MADS box protein a
12	385	31.7	212	2 S31707	floral homeotic pr
13	385	31.7	212	2 S60268	FBP3 protein - gar
14	347.5	28.6	215	2 S28062	homeotic protein g
15	340.5	28.0	209	2 S35226	homeotic protein g
16	331.5	27.3	210	2 A53839	B function floral
17	326	26.8	210	2 U01689	floral binding pro
18	313	25.7	210	2 T03902	MADS4 box protein
19	306.5	25.2	209	2 T03894	MADS box protein -
20	301	24.8	249	2 T04335	MADS box protein -
21	298	24.5	249	2 T04307	M79 protein - rice
22	296.5	24.4	221	2 T09347	MADS box protein A
23	295	24.3	251	2 T04169	MADS box protein -
24	291	23.9	231	2 T14801	MADS box protein W
25	288.5	23.7	228	2 T05621	MADS box protein A
26	287	23.6	248	2 T04170	MADS box protein -
27	283.5	23.3	224	2 J01690	MADS box protein f
28	281	23.1	227	2 H84614	probable MADS-box
29	281	23.1	250	2 T04167	MADS box protein -

30	280.5	23.1	247	2 S78015	MADS box protein D
31	280.5	23.1	250	2 D39534	MADS box protein A
32	280.5	23.1	251	2 T00656	MADS box protein A
33	280.5	23.1	256	2 T45817	MADS transcription
34	280.5	23.1	261	2 T09603	MADS-box protein 3
35	280	23.0	242	2 S71208	MADS box protein 1
36	280	23.0	246	2 T17023	MADS box protein A
37	280	23.0	252	2 F39534	floral homeotic pr
38	280	23.0	254	2 T10467	MADS box protein D
39	279.5	22.9	261	2 S51935	probable MADS-box
40	279	22.9	246	2 E39534	floral homeotic pr
41	279	22.9	248	2 S20886	MADS box protein s
42	279	22.9	258	2 G84858	floral homeodomain
43	278	22.9	262	2 T08039	MADS-box protein -
44	277.5	22.8	243	2 S71756	MADS box protein D
45	277	22.8	233	2 T10714	MADS-box protein C

ALIGNMENTS

RESULT 1

S23731 MADS box protein TDR6 - tomato (fragment)

N/Alternate names: floral homeotic protein TM6

C/Species: Lycopersicon esculentum (tomato)

C/Date: 27-May-1994 #sequence_revision 26-May-1995 #text_change 26-Aug-1999

C/Accession: S23731, S38778

R/Punell, L.; Abu-Abeid, M.; Zamir, D.; Nacken, W.; Schwarz-Sommer, Z.; Lifschultz, E. Plant J. 1, 255-266, 1991

A/Title: The MADS box gene family in tomato: temporal expression during floral development

A/Reference number: S23728, PMID:93251098, PMID:1688249

A/Accession: S23731

A/Molecule type: mRNA

A/Residues: 1-222 <PNU>

A/Cross-references: EMBL:X60759

R/Punell, L. submitted to the EMBL Data Library, July 1991

A/Reference number: S38778

A/Accession: S38778

A/Molecule type: mRNA

A/Residues: 1-159, 'T', 161-222 <PNU>

A/Cross-references: EMBL:X60759; NID:g19385; PID:g19386

C/Genetics:

A/Map position: 2 C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homolog

C/Keywords: DNA binding; nucleus; transcription regulation F,1-54/Domain: serum response factor DNA-binding domain homology (fragment) <SRF>

Query Match Best local similarity 57.3%; Score 696.5; DB 2; Length 222; Matches 139; Conservative 29; Mismatches 52; Indels 11; Gaps 4;

QY	4	GKIEIKLQNIQNRQVYTKRRNGIFPKAQLTLCDAVSLIMSNKKMREHYISPTT	63
DB	1	GKIEIKKIKSNTSRQVYTKRRNGIFPKKKEKTLVCDAKISIMLSSTKRYEYSPNT	60
QY	64	TKSMYDQYKQMGIDMRTHSESMKDTLWKLKEINNKLRERIRORGLHNGASPELAS	123
DB	61	TKSMIDQYQALGVDSIHSEKMGKLNKLEINNKLRERIRORGLHNGASPELAS	120
QY	124	LDDEQSSLDAIRQRKRYIKTQTEITKKRVNLEGRNMTLHGFDQAPAGDPQYGE	183
DB	121	LQNIITESVAIERKRYIKTQTEITKKRVNLEGRNMTLHGFDQAPAGDPQYGE	177
QY	184	DNEGDESSALALNSGANNLYTHLH--HPLHHGSSLSGSIHLHLRLA	232
DB	178	ENEGHYSAVAFANGVHNLVAFRLQPLHPLNNEG--GFGS-----RDLRLS	222

RESULT 2

S12378 MADS box protein defa-1 - garden snapperagon

N/Alternate names: gene deficiencies protein
 C/Species: Antirrhinum majus (garden snapdragon)
 C/Date: 21-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 21-Jul-2000
 C/Accession: S12378; S19232
 R/Schwarz-Sommer, H.; Beltrani, J.P.; Huijser, P.; Pape, H.; Loennig, W.E.; Saedler, H.; Schwarz-EMBO J. 9, 605-613, 1990
 A/Title: Deficiens, a homeotic gene involved in the control of flower morphogenesis in A
 A/Reference number: S12378; MUID:90183955; PMID:1968830
 A/Accession: S12378
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-227 <SOM>
 A/Cross-references: GB:X52023; NID:g16019; PIDN:CAA36268.1; PID:g16020
 R/Schwarz-Sommer, Z.; Hue, I.; Huijser, P.; Flor, P.J.; Hansen, R.; Teters, F.; Loennig, EMBO J. 11, 221-263, 1992
 A/Title: Characterization of the Antirrhinum floral homeotic MADS-box gene deficiencies: ev
 A/Reference number: S19232; MUID:92155166; PMID:1346760
 A/Accession: S19232
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-227 <SCH>
 A/Cross-references: EMBL:X62810; NID:g16017; PIDN:CAA44629.1; PID:g16018
 C/Genetics:
 A/Gene: deficiencies
 A/Intons: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
 C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 C/Keywords: DNA binding; nucleus; transcription regulation
 F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 54.9%; Score 667.5; DB 2; Length 227;
 Best Local Similarity 56.4%; Pred. No. 9.3e-41;
 Matches 128; Conservative 37; Mismatches 53; Indels 9; Gaps 3;

1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKHXYISP 60
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 1 MARGKIQIKRIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKHXYISP 60

QY 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120
 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120
 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120

Db 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120
 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120
 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120

QY 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180
 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180
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Db 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180
 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180
 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180

QY 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224
 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224
 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224

Db 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224
 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224
 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224

RESULT 3
 S31693
 MADS box protein gp - garden petunia
 N/Alternate names: floral homeotic protein gp; transcription factor gp
 C/Species: Petunia x hybrida (garden petunia)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Sep-1999
 C/Accession: S31693
 R/Kush, A.; Brumelle, A.; Shevell, D.; Chua, N.H.
 submitted to the EMBL Data Library, November 1992
 A/Description: Nucleotide sequence and expression pattern of two genes encoding MADS box
 A/Reference number: S31693
 A/Accession: S31693
 A/Molecule type: mRNA
 A/Residues: 1-231 <KUS>
 A/Cross-references: EMBL:X69946; NID:g22664; PID:g22665
 C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation
 F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 52.8%; Score 641.5; DB 2; Length 231;
 Best Local Similarity 55.6%; Pred. No. 6.9e-39;
 Matches 129; Conservative 36; Mismatches 52; Indels 15; Gaps 4;

QY 1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKHXYISP 60
 1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKHXYISP 60
 1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKHXYISP 60

Db 1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKHXYISP 60
 1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKHXYISP 60
 1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKHXYISP 60

QY 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120
 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120
 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120

Db 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120
 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120
 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120

QY 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180
 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180
 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180

Db 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180
 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180
 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180

QY 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224
 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224
 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224

Db 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224
 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224
 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224

RESULT 4
 T07066
 MADS-box protein homolog DEF4 - potato
 N/Alternate names: deficiencies analogue
 C/Species: Solanum tuberosum (potato)
 C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
 C/Accession: T07066
 R/Garcia-Maroto, F.; Salami, F.; Rohde, W.
 Plant J. 4, 771-780, 1993
 A/Title: Molecular cloning and expression patterns of three alleles of the Deficiens-hom
 A/Reference number: Z15896; MUID:94100991; PMID:7903890
 A/Accession: T07066
 A/Status: preliminary; translated from GB/EMBL/DD3J
 A/Molecule type: DNA
 A/Residues: 1-228 <GAR>
 A/Cross-references: EMBL:X67511; NID:g431225; PIDN:CAA78446.1; PID:g431226
 A/Experimental source: cv. Granola; leaf
 A/Genetics:
 A/Gene: def4
 A/Intons: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
 C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
 C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation
 F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 51.7%; Score 628.5; DB 2; Length 228;
 Best Local Similarity 54.1%; Pred. No. 5.6e-38;
 Matches 124; Conservative 40; Mismatches 54; Indels 11; Gaps 3;

1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKHXYISP 60
 1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKHXYISP 60
 1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKHXYISP 60

Db 1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKHXYISP 60
 1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKHXYISP 60
 1 MARGKIEIKLIENQTNQVYTSKRNGIFPKAQLTVLCAKYSILMLSTNKHXYISP 60

QY 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120
 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120
 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120

Db 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120
 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120
 61 TTTKSMYDDYQKTMGIDLWRTHEESKMDTLWKLKEINNKLRREIRORLGHDLNGISFDE 120

QY 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180
 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180
 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180

Db 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180
 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180
 121 LASLDDMOSSLDAIRORXHVITKQETETTKKKVKNLEQRGNMLHGYFDOEAAGEDPQY 180

QY 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224
 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224
 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224

Db 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224
 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224
 181 GYEDNEGDYSSALALSGANNLYTFHL---HHPNHLHGSSLSGSSIT 224

RESULT 5
 T07410
 MADS box protein homolog DEF2 - potato
 N/Alternate names: deficiencies analogue
 C/Species: Solanum tuberosum (potato)
 C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 03-Dec-1999
 C/Accession: T07410
 R/Garcia-Maroto, F.
 submitted to the EMBL Data Library, August 1992
 A/Reference number: Z16019
 A/Accession: T07410

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-228 <GAR>
A:Cross-references: EMBL:X67508; NID:G511064; PIDN:CAA47845.1; PID:G511065
A:Experimental source: cv. H81.1506/60; dev. stage vegetative; tissue type flower
C:Gene: def2
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding; nucleus; transcription factor; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 51.4%; Score 624.5; DB 2; Length 228;
Best Local Similarity 53.7%; Pred. No. 1.1e-37;
Matches 123; Conservative 41; Mismatches 54; Indels 11; Gaps 3;

QY 1 MARGKIEIKLENTQNRQVTSKRRNGIFPKAQLTLVCDKAVSLIMNTNKKHEIYSP 60
DB 1 MARGKIQIKLENTQNRQVTSKRRNGIFPKAQLTLVCDKAVSLIMNTNKKHEIYSP 60
QY 61 TTTTSMYDYOXTMGIDLMRTHEESMKDTLWKLEINNKLRREIRORLGHDLNGLSFE 120
DB 61 SITTNNLEFDLYOKTIGVDIMTSYERKQEQRLKLDVVRNLRKEIRORMGESLNDLNFQ 120
QY 121 LASLDDENQSSLDLIRORRKHVITKTOTETTKKKVKNLEQRGNMLHGYPQEAAGEPQY 180
DB 121 LEEIMENVNLSLKLIRERKRVIGNQLETYRKRVNVEEIHRLNLEFDAQEDPYG 177
QY 181 GYEDNEGDEYSALALNSGANNLYTFHL-----HHNPLHGSSSGSSIT 224
DB 178 GLVNGEDGYNSVLGPRPTGHHIILALGLQPNNNHHHLSGCGSDIT 223

RESULT 6
T09335
MADS-box protein NMH 7 - alfalfa
C:Species: Medicago sativa (alfalfa)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Dec-1999
C:Accession: T09335
R:Kitby, C.; Heard, J.; Carroll, S.; Leshner, J.; Ganter, G.; Dunn, K.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z16647
A:Accession: T09335
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-229 <KIR>
A:Cross-references: EMBL:AF042068; NID:G2827299; PID:G2827300
A:Experimental source: strain Itroquois; root nodules
C:Gene: nmh 7
A:Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 51.0%; Score 620.5; DB 2; Length 229;
Best Local Similarity 54.0%; Pred. No. 2.2e-37;
Matches 122; Conservative 36; Mismatches 63; Indels 5; Gaps 2;

QY 1 MARGKIEIKLENTQNRQVTSKRRNGIFPKAQLTLVCDKAVSLIMNTNKKHEIYSP 60
DB 1 MARGKIQIKLENTQNRQVTSKRRNGIFPKAQLTLVCDKAVSLIMNTNKKHEIYSP 60
QY 61 TTTTSMYDYOXTMGIDLMRTHEESMKDTLWKLEINNKLRREIRORLGHDLNGLSFE 120
DB 61 SASTQPFDPQYQMTYIGIDLMNSHYENQENLKKLDVVRNLRKEIRORMGESLNDLNSGE 120
QY 121 LASLDDENQSSLDLIRORRKHVITKTOTETTKKKVKNLEQRGNMLHGYPQEAAGEPQY 180
DB 121 LRLLEDENQSSLDLIRORRKHVITKTOTETTKKKVKNLEQRGNMLHGYPQEAAGEPQY 177
QY 181 GYEDNEGDEYSALALNSGANNLYTFHL--HPNPLHGSSSGSSIT 224
DB 178 EMDNGGEYSVIGSNLGRMFALSLQPTPHNPNNGASAAADLT 223

RESULT 7
A42095
floral homeotic protein APETALA3 (AP3) - Arabidopsis thaliana
N:Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A42095; S52633; T47593
R:Jadick, T.; Brockman, L.L.; Meyerowitz, E.M.
Cell 68, 683-697, 1992
A:Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and its ex
A:Reference number: A42095; NCID:92154682; PMID:1346756
A:Accession: A42095
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-232 <JAC>
A:Cross-references: GB:M86357; NID:G166607; PIDN:AAA32740.1; PID:G166608
A:Experimental source: petals, stamens
A:Note: Sequence extracted from NCBI Backbone (NCBI:82520, NCBI:82521)
R:Okamoto, H.; Yano, A.; Shirasahi, H.; Okada, K.; Shimura, Y.
Plant Mol. Biol. 26, 465-472, 1994
A:Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabid
A:Reference number: S52633; NCID:95036018; PMID:7948893
A:Accession: S52633
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-63 <OKA>
A:Cross-references: GB:D21125
R:Blocker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat M.; Mewes,
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24469
A:Accession: T47593
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <BLO>
A:Cross-references: EMBL:AL132971
A:Experimental source: cultivar Columbia; BAC clone T12E18
C:Gene: nmh 3
A:Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding; nucleus; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 46.4%; Score 564; DB 2; Length 232;
Best Local Similarity 52.8%; Pred. No. 2.4e-33;
Matches 113; Conservative 31; Mismatches 66; Indels 4; Gaps 2;

QY 1 MARGKIEIKLENTQNRQVTSKRRNGIFPKAQLTLVCDKAVSLIMNTNKKHEIYSP 60
DB 1 MARGKIQIKLENTQNRQVTSKRRNGIFPKAQLTLVCDKAVSLIMNTNKKHEIYSP 60
QY 61 TTTTSMYDYOXTMGIDLMRTHEESMKDTLWKLEINNKLRREIRORLGHDLNGLSFE 120
DB 61 NTTTKEIVDLYQTSIDVWATQYERMQETKLTETNNLTLQIKORLGECIDELDIOE 120
QY 121 LASLDDENQSSLDLIRORRKHVITKTOTETTKKKVKNLEQRGNMLHGYPQEAAGEPQY 180
DB 121 LRLLEDENQSSLDLIRORRKHVITKTOTETTKKKVKNLEQRGNMLHGYPQEAAGEPQY 177
QY 181 GYEDNEGDEYSALALNSGANNLYTFHLHPNHL 214
DB 178 GLVNGEDGYNSVLGQIEGSAVALRPHQ-NHHH 210

RESULT 8
T14473
MADS box protein 2AP3 - broccoli
N:Alternate names: homeotic protein 2AP3
C:Species: Brassica oleracea var. botrytis (broccoli)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000

Query Match	41.28;	Score 500.5;	DB 2;	Length 203;
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```
Query Match      41.2%; Score 500.5; DB 2; Length 203;
```

Best Local Similarity 48.0%; Pred. No. 7.2e-29;
Matches 98; Conservative 41; Mismatches 54; Indels 11; Gaps 3;

QY 26 NGIPKKAQELTVLCDAKVSLIMLNTNMGHEIYIPPTTTTSMYDYQRTMGIDIMLRHHE 85
 Db 1 NGEPKKAQELTVLCDAKVSIYMISTGKMHFISPSITTKQLPULYKXTIGVDIMTWTHYE 60
 QY 86 SMKDTLWLKKEINNKLRREIRQRLGHDINGISFDELASLDDEMOSLIDAIRQKRTVIKT 145
 Db 61 KMQQLRKTKDVNNENLRREIRQRMGESINDINYEQLTEIEMENVDSNKLIRERAFKIGN 120
 QY 146 QTEITTKKKVKVLEQRGKMLHGYPDOEAGSDPQYGYEDNMGDVSLLALNSGANNLYTF 205
 Db 121 QIEIYTRKKVRNVEINRNL---LEFDARQEDPVGGLVEHDGYNSVYLGFPFGPRILLDL 177
 QY 206 HL-----HHPIHLHGSSSLGSSIT 224
 Db 178 RLQPPNNYHNHLHSG---GSDIT 198

```

RESULT 12
S31707
floral homeotic protein pmad2 - garden petunia
N:Alternate names: MADS box-containing protein; transcription factor pmad2
C:Species: Petunia x hybrida (garden petunia)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 03-Dec-1999
C:Accession: S31707
R:Kush, A.; Brunelle, D.; Chua, N.H.
submitted to the EMBL Data Library, November 1992
A:Description: Nucleotide sequence and expression pattern of two genes encoding MADS box
A:Reference number: S31693
A:Accession: S31707
A:Molecule type: mRNA
A:Residues: 1-212 <KUS>
A:Cross-references: EMBL:X63947; NID:Q22666; PID:Q22667
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain
C:Keywords: DNA binding; nucleus; transcription factor; transcription regulation
F:2-57/domain: serum response factor DNA-binding domain homology <SRF>

Query Match      31.7%; Score 385; DB 2; Length 212;
Beet Local Similarity 37.9%; Pred. No. 1.4e-20;
Matches 85; Conservative 40; Mismatches 73; Indels 26; Gaps 4;

```

```

QY 1 MARGIEIKLENNQNRNVRYSKRRNGIFPKAQOEITVLCDAKVSILMISNNKHIEISP 60
Dh 1 MGRGIEIKRELENSNRQVYTSKRRNGIIKAKETIVLCDAKVSILIIKNGSGKHIEYCSF 60
QY 61 TTTTSMYDDYQKTMGIDLMRTHESMKDTLMKLEINNKLRREIRQRLGHDNLGSLFDE 120
Dh 61 STTLPLMDMGYQKTSGRRLMDAKHEHLSNEIDRIKKEENDMQVYLRHLKSGEDINSLNKHE 120
QY 121 LASLDDMQSSLDAIRQKRHVIKTQETTKKKYKVNLEFORGNMLHGFDEEAGE---- 176
Dh 121 LMVLEEGGLNGLSISIAQOSEILR---MVRKNQOILIEEBKHQOYALAHQEKAMAGGNNM 176
QY 177 ---DPQGYEDNEGDYESALALNSGANNLYTFHLH---HFNLLH 213
Dh 177 RMIEVYHQDRDDEYEQ-----MPBALRVQPMQPVLLH 209

```

RESULT 13
S60288
FBP3 protein - garden petunia
C[Species: Petunia x hybrida (garden petunia)
C[Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jul-2000
C[Accession: S60288
R[angement: G.C.; Franken, J.; Buscher, M.; Weiss, D.; van Tunen, A.J.
Plant J. 5, 33-44, 1994
A[Title: Co-suppression of the petunia homeotic gene fbp2 affects the identity of the
A[Reference number: S60288; MUID:94177174; PMID:7907515
A[Status: preliminary
A[Molecule type: mRNA

A;Residues: 1-212 <ANG>
A;Cross-references: EMBL:X17147; NID:q454264; PDB:CA50549.1; PID:q454265
C;Superfamily: transcritpion factor squa; serum response factor DNA-binding domain homology
E;2-57/Domain: serum response factor DNA-binding domain homology <SRE>

```

Query Match      31.7%; Score 385; DB 2; Length 212;
Best Local Similarity 37.9%; Pred. No. 1; 48 20;
Matches 85; Conservative 40; Mismatches 73; Indels 26; Gaps 4;

QY      1  MARGKIEIKLIENQNRQVTTYKRRNGIFPKYAQELTVLCDAYSLIMLSNTKKEHEIYSP 60
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  MGRGKIEIKRIENSSNRQVTTYKRRNGIIKKKKEITVLCDAVSYLIIFNSSGKMEHCSP 60

QY      61  TTTTTSKYDDQYKTMWIDLMRTHEESMKDTLWAKLEINNKLRREIRORLGHNLGSLPDE 120
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61  STLLPMLDQYQGTISGRRLMDAKHEVLSNEIDRIKENQSMQYKRLHMGEDINSLNHKE 120

QY      121  LASLIDEMOSSLDAIQRKTHVYIKTQTEYTKKVKYKNLEQRGNMTHGYDDQZAAE--- 176
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121  LMTLEBETLNGLSSISAKOSEIIR---IVRXNDQDLEEBHKQLOYALHOKEMAMWGMM 176

QY      177  ---DPOGYEDNEGDEYSALALNSGANNTYTFHL---HPNIIH 213
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      177  RMIEEYTHQGRDRDEYQ-----MPALRYQRPWQPIYH 209

```

RESULT 14
S28062
homeotic protein globose - garden snapperagon
C:Species: Antirrhinum majus (garden snapperagon)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #ext_change 21-Jul-2000
C/Accession: S28062
R/Ritterbein, W.; Ramirez, L.; Motte, P.; Hue, I.; Huisser, P.; Loennig, W.E.; Seidler, H.
EMBO J. 11, 4693-4704, 1992
A>Title: GLOBOSA: a homeotic gene which interacts with DEFTENS in the control of Antirrhinum
A/Reference number: S28062; M0ID:93098442; PMID:1511166
A/Accession number: S28062
A/Molecule type: DNA
A/Residues: 1-215 <RPO>
A/Cross-references: EMBL:X68831; NID:g16023; PIDN:CAA48725.1; PID:g16024
C/Genetics:
A/Gene: glo
A/Introns: 63/2; 85/3; 106/2; 139/3; 149/3; 164/3
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C/Keywords: DNA binding; nucleus; transcription regulation
/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match	28.64%	Score 347.5	DB 2	Length 215
Best Local Similarity	34.18%	Pred. No. 6.7e-18		
Matches	77	Conservative 49	Mismatches 71	Indels 29
			Gaps	5
QY	1	MARGKEIKLIENQTNROVYTSRRNGIEFKAGELTVLCDAYSLIMLSNTNKGHEIYSP	60	
DB	1	MGRGKIKIKIENSNRQVYTSRRRNGIMKKAKEIIVLCDAHVSIIIFASSGCMHEFCSP	60	
QY	61	TTTTKSYDDYQKTMGIDILWRTHESBKKDILMTKLKSNKKLRREIRQRGHDANGSPSP	120	
DB	61	STTVLVLDLHYHKLSGKRLNDPKHEHLDNEINRVKKNDSMQIELHNLKGEDITLTINAYE	120	
QY	121	LASLDDEGSSLDAIRQKRYHVIK-----TQETTKKKYKNLEQRRGNALHGY	168	
DB	121	LMVLVEDALENGTSATKKQWEPVRRMRKHNENWEENEQSLQFRLRQWHLDPMDNDVM---	177	
QY	169	FDQRAAGEDPQGYGDNEDGESALALSNGANLVTYFNHL--HPNL 212		
DB	178	-ESCAVYD---HHNHQNIADYEKQMP-----FAFRVQPMQPNL 211		

RESULT 15
S35226
homeotic protein globosa homolog - common tobacco
C:Species: Nicotiana glauca (common tobacco)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 09:11:24 ; Search time 15.5705 Seconds
(without alignments)
775.845 Million cell updates/sec

Title: US-10-069-527-4
Perfect score: 1216
Sequence: 1 MARGIKIKIENQTRQVT.....HHGSSLSGSSITHLHDLRLA 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	667.5	54.9	227	1	DEFA_ANTMA
2	641.5	52.8	231	1	MAD1_PETTY
3	564	46.4	232	1	AP3_ARATH
4	549	45.1	214	1	CMB2_DIAA
5	385	31.7	212	1	MAD2_PETTY
6	350.5	28.8	237	1	M13_GNEGN
7	347.5	28.6	215	1	GLOB_ANTMA
8	340.5	28.0	209	1	GLOB_TOBAC
9	332	27.3	259	1	M17_MAIZE
10	331.5	27.3	208	1	P1ST_ARATH
11	326	26.8	210	1	PBP1_PETTY
12	320.5	26.4	252	1	TT16_ARATH
13	307	25.2	247	1	P324_PETTY
14	297.5	24.5	247	1	DE21_ANTMA
15	296.5	24.4	221	1	AG14_ARATH
16	295	24.3	241	1	AG19_PETTY
17	288.5	23.7	228	1	AG17_ARATH
18	285	23.4	265	1	AG18_ARATH
19	283	23.3	241	1	AG18_SINLA
20	281	23.1	227	1	AG17_ARATH
21	280.5	23.1	250	1	SEB2_ARATH
22	280.5	23.1	251	1	SEB3_ARATH
23	280	23.0	242	1	AG18_ARATH
24	280	23.0	252	1	AG16_ARATH
25	280	23.0	254	1	AG19_SINLA
26	279	22.9	246	1	AG15_ARATH
27	277	22.8	233	1	CMB1_DIAA
28	276	22.7	268	1	AG15_ARATH
29	275.5	22.7	224	1	AG19_LYCES
30	275	22.6	227	1	AG18_LYCES
31	274	22.5	250	1	AG19_ARABE
32	271.5	22.3	251	1	SEB1_ARATH
33	270.5	22.2	253	1	CAL_ARATH

34	270	22.2	244	1	AG13_ARATH	Q38837 arabidopsis
35	269.5	22.2	242	1	SOCI_ARATH	Q64645 arabidopsis
36	269.5	22.2	242	1	AG_PANCI	Q40872 panax ginseng
37	268	22.0	258	1	AG13_ARATH	P29383 arabidopsis
38	267	22.0	219	1	AG19_ARATH	O82743 arabidopsis
39	265	21.8	230	1	AG11_ARATH	Q38836 arabidopsis
40	265	21.8	248	1	AG11_ARATH	P29381 arabidopsis
41	264	21.7	250	1	AG18_SOLCO	Q22328 solanum com
42	262.5	21.6	250	1	AG18_SOLTU	Q42429 solanum tub
43	261	21.5	248	1	AG_TOBAC	Q43585 nicotiana t
44	260.5	21.4	248	1	AG_LYCES	Q40168 lycopersico
45	260.5	21.4	252	1	AG_ARATH	P17839 arabidopsis

ALIGNMENTS

RESULT 1	ID	DEFA_ANTMA	STANDARD;	PRT;	227 AA.
AC	P23706;				
DT	01-NOV-1991 (Rel. 20, Created)				
DT	01-NOV-1991 (Rel. 20, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Floral homeotic protein DEF1.				
GN	DEFA.				
OS	Antirrhinum majus (Garden snapdragon).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;				
OC	Lamiales; Antirrhinaceae; Antirrhineae; Antirrhinum.				
OX	NCBI_TaxID=4151;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90183955; PubMed=1968830;				
RA	Sommer H., Beltan J.-P., Huijser P., Pape H., Loeenig W.-E.,				
RA	Saedler H., Schwarz-Sommer Z.;				
RT	"Deficiens, a homeotic gene involved in the control of flower				
RT	morphogenesis in Antirrhinum majus: the protein shows homology to				
RT	transcription factors."				
RL	EMBO J. 9:605-613(1990).				
RP	SEQUENCE FROM N.A.				
RC	STRATIN=cy. Sipe 50;				
RX	MEDLINE=9215166; PubMed=1346760;				
RA	Schwarz-Sommer Z., Hue I., Huijser P., Flor P.J., Hansen R.,				
RA	Teters F., Loeenig W.-E., Saedler H., Sommer H.;				
RT	"Characterization of the Antirrhinum floral homeotic MADS-box gene				
RT	deficiens: evidence for DNA binding and autoregulation of its				
RT	persistent expression throughout flower development."				
RL	EMBO J. 11:251-263(1992).				
CC	- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF				
CC	- FLOWER DEVELOPMENT. ACTS IN CONJUNCTION WITH GLOBOSA (GLO).				
CC	- SUBCELLULAR LOCATION: Nuclear.				
CC	- MISCELLANEOUS: MUTATIONS IN DEFA CAUSE TRANSFORMATION OF PETALS				
CC	INTO SEPALs AND STAMINA INTO CARPels.				
CC	- SIMILARITY: Contains 1 MADS-box domain.				
CC	- SIMILARITY: Contains 1 MADS-box domain.				
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	EMBL; X52023; CAA36268.1; -				
DR	EMBL; X62810; CAA44629.1; -				
DR	PIR; S12378; S12378.				
DR	HSSP; P11746; 1MM.				
DR	TRANSFAC; T01008; -				
DR	InterPro; IPR002487; TF_Kbox.				
DR	InterPro; IPR002100; TF_MADSbox.				

DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRP-TF; 1.
 DR PRINTS: PR00404; MADS-DOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KW Developmental protein.
 FT DOMAIN 3 MADS-box.
 FT DOKAIN 93 165
 SQ SEQUENCE 227 AA; 26279 MW; 95E3FF60924FDEBD CRC64;
 Query Match 54.9%; Score 667.5; DB 1; Length 227;
 Best Local Similarity 56.4%; Pred. No. 6.6e-41;
 Matches 126; Conservative 37; Mismatches 53; Indels 9; Gaps 3;
 Oy 1 MARKIKIKLENOTNQVTSKRRNGIFKKAOELTVLCAKYSIMLSTNKNMHEYISP 60
 Db 1 MARKIKIKLENOTNQVTSKRRNGIFKKAOELTVLCAKYSIMLSTNKNMHEYISP 60
 Oy 61 TTTKSMYDYQKTMGIDLMRTHEESMKOTLMKLEINNKLRREIRQLGHDINGLSFDE 120
 Db 61 TTTAKQIFDQYQAVGVDLMSHYEKQEHKTLKLNVRNLRREIRQLGHDINGLSFDE 120
 Oy 121 LASIDDEMGSLLAIRQKTHVITQTETTKKKYKNLEQRGNMLHGFDQEAAGEPQY 180
 Db 121 IVNLIEMDNLSLKIRERKRYVISMNQIDTSKKRYVNEEIRNLV--LEFDARREDPAF 177
 Oy 181 GYEDNEGDESSALASNGANNLYTFHL--HHNPLHHGSSIGSSIT 224
 Db 178 GLVDEGDNYSVLGFPNGRRIALRLPTNHHPTLHSGG--GSDIT 221

RESULT 2
 ID MADI_PETHY STANDARD; PRT; 231 AA.
 AC C07472;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Floral homeotic protein PMA51 (Green petal homeotic protein).
 GN PMA51 OR GP.
 OS Petunia hybrida (Petunia).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Petunia.
 ON NCBI_TaxID=4102;
 RX MEDLINE=94105323; PubMed=8278527;
 RA Kunh A., Brunelle A., Shevell D., Chua N.-H.;
 RL Plant Physiol. 102:1051-1052(1993).
 CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
 CC FLOWER DEVELOPMENT. NECESSARY FOR THE NORMAL DEVELOPMENT OF
 CC PETALS. ABSENCE OF THE PMA51 PROTEIN CAUSES TRANSFORMATION OF
 CC PETALS INTO SEALS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: Predominantly expressed in petals and stamens,
 CC less in carpels and sepals.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 CC -----
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 CC -----
 DR EMBL, X63946; CAA49567.1; --

DR PIR: S31693; S31693.
 DR HSSP: P11746; 1MMN.
 DR TRANSFAC: T01777; --
 DR InterPro: IPR002487; TF_Kbox.
 DR InterPro: IPR002100; TF_MADSbox.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRP-TF; 1.
 DR PRINTS: PR00404; MADS-DOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Activator; Nuclear protein;
 FT Developmental protein.
 FT DOMAIN 3 MADS-box.
 FT DOKAIN 93 165
 SQ SEQUENCE 231 AA; 27039 MW; 76A5E0B3486B6F CRC64;
 Query Match 52.8%; Score 641.5; DB 1; Length 231;
 Best Local Similarity 55.6%; Pred. No. 4.8e-39;
 Matches 129; Conservative 36; Mismatches 52; Indels 15; Gaps 4;
 Oy 1 MARKIKIKLENOTNQVTSKRRNGIFKKAOELTVLCAKYSIMLSTNKNMHEYISP 60
 Db 1 MARKIKIKLENOTNQVTSKRRNGIFKKAOELTVLCAKYSIMLSTNKNMHEYISP 60
 Oy 61 TTTKSMYDYQKTMGIDLMRTHEESMKOTLMKLEINNKLRREIRQLGHDINGLSFDE 120
 Db 61 SITTKQIFDQYQAVGVDLMSHYEKQEHKTLKLNVRNLRREIRQLGHDINGLSFDE 120
 Oy 121 LASIDDEMGSLLAIRQKTHVITQTETTKKKYKNLEQRGNMLHGFDQEAAGEPQY 180
 Db 121 LELMENVDNLSLKIRERKRYVISMNQIDTSKKRYVNEEIRNLV--LEFDARREDPAF 176
 Oy 181 GYEDNEGDESSALASNGANNLYTFHL--HHNPLHHGSSIGSSIT 224
 Db 177 GLVEGEGDNYSVLGFPNGRRIALRLQPNHGHQNHHLHSGG--GSDIT 225

RESULT 3
 ID AP3_ARATH STANDARD; PRT; 232 AA.
 AC P35632; Q39003; Q8LB79; Q9S703; Q9S014; Q9S015; Q9S016; Q9S017;
 AC Q95018; Q9S019; Q9S020; Q9S021; Q9S022; Q9S023; Q9S024;
 DT 01-JUN-1994 (Rel. 28, Created)
 DT 01-JUN-1994 (Rel. 28, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Floral homeotic protein APETALA3.
 GN AP3 OR AT3G54340 OR T12E18.30.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eusterales II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_TaxID=3702;
 RX MEDLINE=92154682; PubMed=1346756;
 RA Jack T., Brockman L.B., Meyerowitz E.M.;
 RL "The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS
 RL box and is expressed in petals and stamens.";
 RL Cell 68:683-697(1992).
 CC -----
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 CC -----
 DR EMBL, X63946; CAA49567.1; --

RC cv. Chi-1, cv. Co-1, cv. Columbia, cv. Corsacalla-1, cv. Cvi-0,
RC cv. Gr-3, cv. J1-1, cv. Kas-1, cv. Kent, cv. Landsberg erecta,
RC cv. Li-3, cv. Li-8, and cv. Lisea;
RX MEDLINE=99126449; PubMed=9927474;
RA Putugnanan M.D., Suddith J.I.;
RT "Molecular population genetics of floral homeotic loci: departures
RT from the equilibrium-neutral model at the *APETALA3* and *PISTILLATA*
RT genes of Arabidopsis thaliana";
RL Genetics 151:839-848(1999).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Anseorge W., Unsel'd M.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaler B.,
RA Delany M., Boutry M., Grievell L.A., Maché R., Pulgumenech P.,
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Queirer F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurbach E., Dirzner H., Erile H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelico M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bagnies M., Terol J., Clement J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Liauro C., Purnelle B., Masny D.,
RA de Haan M., Maere A., Alcaraz J.-P., Cottet A., Casacubeta E.,
RA Monfort A., Agirretxu A., Flores M., Lignori R., Vitale D.,
RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mews H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Uteback T., Fujii C.Y., Shea T.P.,
RA Cressy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Miltschew J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Frazer C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara T., Matsunoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shimo S., Takeuchi C., Wada T.,
RA Marumae A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana";
RL Nature 408:820-822(2000).
[5]
RP SEQUENCE FROM N.A.
RA Brover V., Trukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.A.;
RT "Full-length cDNA from Arabidopsis thaliana";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954650; PubMed=14593172;
RA Yamada K., Lim J., Dale J.M., Chen H., Shim P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Mizunda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA Akawa T., Banth J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao O., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Heuan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamuya A., Meyers C., Nakajima M., Natsuka M., Seki M., Sakurai T.,
RA Satou M., Tame R., Vayberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
RT genome";
RL Science 302:842-846(2003).
[7]
RP SEQUENCE OF 36-128 FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=99311297; PubMed=10382288;
RA Brunel D., Froger N., Pelletier G.;
RT "Development of amplified consensus genetic markers (ACGM) in Brassica

RT napus from Arabidopsis thaliana sequences of known biological
RT function";
RL Genome 42:387-402(1999).
[8]
RP FUNCTION.
RX MEDLINE=96152196; PubMed=8565821;
RA Krizek B.A., Meyerowitz E.M.;
RT "The Arabidopsis homeotic genes *APETALA3* and *PISTILLATA* are sufficient
RT to provide the B class organ identity function";
RL Development 122:11-22(1996).
[9]
RP CHARACTERIZATION.
RX MEDLINE=96209811; PubMed=8643482;
RA Riechmann J.L., Krizek B.A., Meyerowitz E.M.;
RT "Dimerization specificity of Arabidopsis MADS domain homeotic proteins
RT *APETALA1*, *APETALA3*, *PISTILLATA*, and *AGAMOUS*";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).
[10]
RP GENETIC REGULATION.
RX MEDLINE=21178805; PubMed=11283333;
RA Ng M., Yanofsky M.F.;
RT "Activation of the Arabidopsis B class homeotic genes by *APETALA1*";
RL Plant Cell 13:739-753(2001).
[11]
RP CHARACTERIZATION.
RX MEDLINE=21074934; PubMed=11206550;
RA Homma T., Goto K.;
RT "Complexes of MADS-box proteins are sufficient to convert leaves into
RT floral organs";
RL Nature 403:525-529(2001).
-1- FUNCTION: Probable transcription factor involved in the genetic
control of flower development. Is required for normal development
of petals and stamens in the wild-type flower. Forms an
heterodimer with *PISTILLATA* that is required for autoregulation of
both *AP3* and *PI* genes. *AP3/PI* heterodimer interacts with *APETALA1*
or *SEPALLATA3* to form a ternary complex that could be responsible
for the regulation of the genes involved in the flower
development.
-1- SUBUNIT: Forms a heterodimer with *PISTILLATA*, capable of binding
to CARG-box sequences. *AP3/PI* heterodimer binds *AP1* or *SEP3* to
form complexes.
-1- SUBCELLULAR LOCATION: Nuclear.
-1- TISSUE SPECIFICITY: Expressed in petals and stamens.
-1- INDUCTION: Positively regulated by the meristem identity proteins
APETALA1 and *LEAFY* with the cooperation of UFO.
-1- MISCELLANEOUS: Mutations in *AP3* cause transformation of petals
into sepals and stamens into carpels.
-1- SIMILARITY: Contains 1 MADS-box dimerization domain.
-1- SIMILARITY: Contains 1 MADS-box domain.

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DR EMBL: M66357; AAA32740.1; -
DR EMBL: D21125; BAA04665.1; -
DR EMBL: AF115798; AAD51887.1; -
DR EMBL: AF115799; AAD51888.1; -
DR EMBL: AF115800; AAD51889.1; -
DR EMBL: AF115801; AAD51890.1; -
DR EMBL: AF115802; AAD51891.1; -
DR EMBL: AF115803; AAD51892.1; -
DR EMBL: AF115804; AAD51893.1; -
DR EMBL: AF115805; AAD51894.1; -
DR EMBL: AF115806; AAD51895.1; -
DR EMBL: AF115807; AAD51896.1; -
DR EMBL: AF115808; AAD51897.1; -
DR EMBL: AF115809; AAD51898.1; -
DR EMBL: AF115810; AAD51899.1; -
DR EMBL: AF115810; AAD51899.1; -

DR EMBL, AF115811; AAD51900.1; -
 DR EMBL, AF115812; AAD51901.1; -
 DR EMBL, AF115813; AAD51902.1; -
 DR EMBL, AF115814; AAD51903.1; -
 DR EMBL, AF132971; CAB81791.1; -
 DR EMBL, AY087369; AAG64919.1; -
 DR EMBL, AY070387; AAG49893.1; -
 DR EMBL, AY142590; AAN13159.1; -
 DR EMBL, AF056541; AAD41557.1; -
 DR PIR, A42095; A42095.
 DR HSSP, P11746; MNM.
 DR TRANSFAC, T01776; -
 DR InterPro, IPR002487; TF_Kbox.
 DR InterPro, IPR002100; TF_MADSbox.
 DR Pfam, PF01486; K-box; 1.
 DR Pfam, PF00319; SRP-TF; 1.
 DR PRINTS, PR00404; MADSDOMAIN.
 DR SMART, SM00432; MADS; 1.
 DR PROSITE, PS00350; MADS_BOX_1; 1.
 DR PROSITE, PS50066; MADS_BOX_2; 1.
 KW Flowering; transcription regulation; Activator; Developmental protein;

Query Match 46.4%; Score 564; DB 1; Length 232;
 Best Local Similarity 52.8%; Pred. No. 1.6e-33;
 Matches 113; Conservative 31; Mismatches 66; Indels 4; Gaps 2;

QY 1 MARGIKIKILENQTNGVYTSKRNGIFPKAQLTYLCAKXSLMLSTNKKHEYISP 60
 DB 1 MARGIKIKILENQTNGVYTSKRNGIFPKAQLTYLCAKXSLMLSTNKKHEYISP 60
 QY 61 TTTTSMYDYOQKTMGIDLRTHESMKDTLMKLEINNKLRREIRQRLGHDLNGLSPDE 120
 DB 61 NTTKKEIVDLVYQTSIDVDWATQYERMQEIKRLLENRLRQIQIRGECJLDELIDICE 120
 QY 121 LASLDDENQSSLDLRQKXHVITQTETTKKVKYKNEFGKGMHGFPOEAGGDPQY 180
 DB 121 LRRLEDEMENTFKLVRRKFKSLQNGQLETTKKKKKSGQDIQKXLIH---ELELRADPPY 177
 QY 181 GYEDNEGDEYASALASNGANNLYTFHLHPHLH 214
 DB 178 GLVNDGDIQSVLQYQTEGSRAYALRPHQ-NHHH 210

RESULT 4
 CMB2_DIACA STANDARD; PRT; 214 AA.

AC Q42498;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE MADS box protein CMB2.
 GN CMB2.
 OS Dianthus caryophyllus (Carnation) (Clove pink).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllaceae; Dianthus.
 OX NCBI_TaxID=3570;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Scanla; TISSUE=Petal;
 RX PubMed=10814815;
 RA Baudinette S.C., Stevenson T.W., Savin K.W.;
 RT "Isolation and characterization of the carnation floral-specific MADS
 box gene, CMB2.";
 RL Plant Sci. 155:123-131(2000).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: In flowers. Not found in vegetative tissues.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
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CC EMBL, L40405; AAB05559.1; -
 CC EMBL, L40805; AAB3903.1; -
 CC PIR, T10715; T10715.
 CC HSSP, P11746; MNM.
 CC TRANSFAC, T03061; -
 CC InterPro, IPR002487; TF_Kbox.
 CC InterPro, IPR002100; TF_MADSbox.
 CC Pfam, PF01486; K-box; 1.
 CC Pfam, PF00319; SRP-TF; 1.
 CC PRINTS, PR00404; MADSDOMAIN.
 CC SMART, SM00432; MADS; 1.
 CC PROSITE, PS00350; MADS_BOX_1; 1.
 CC PROSITE, PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3
 FT DOMAIN 3
 FT DOMAIN 3
 SQ SEQUENCE 214 AA; 24757 MW; ESB8A4013D55D374 CRC64;

Query Match 45.1%; Score 549; DB 1; Length 214;
 Best Local Similarity 51.6%; Pred. No. 1.7e-32;
 Matches 111; Conservative 42; Mismatches 54; Indels 8; Gaps 3;

QY 1 MARGIKIKILENQTNGVYTSKRNGIFPKAQLTYLCAKXSLMLSTNKKHEYISP 60
 DB 1 MARGIKIKILENQTNGVYTSKRNGIFPKAQLTYLCAKXSLMLSTNKKHEYISP 60
 QY 61 TTTTSMYDYOQKTMGIDLRTHESMKDTLMKLEINNKLRREIRQRLGHDLNGLSPDE 120
 DB 61 GYSLKQWYDEYQKIEGVDLRMKQWERMQEQKRYLELNLRLRIRSRMGDLEGLTIVE 120
 QY 121 LASLDDENQSSLDLRQKXHVITQTETTKKVKYKNEFGKGMHGFPOEAGGDPQY 180
 DB 121 LSAIQOEWEBA1101RNNKXHTINQGTTRKIKNLEERTDLV---MELEAKFRGPQF 177
 QY 181 GY-EDNEGDEYASALASNGANNLYTFHL---HHP 210
 DB 178 AIGEDDPNRYEAAAAYGNDVAAANLFAISRHP 212

RESULT 5
 MAD2_PETHY STANDARD; PRT; 212 AA.

AC Q07474;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Floral homeotic protein PMADS 2.
 GN PMADS2.
 OS Petunia hybrida (Petunia).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Petunia.
 OX NCBI_TaxID=4102;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Petal;
 RX MEDLINE=94105323; PubMed=8278527;
 RA Kush A., Brumelle A., Shevell D., Chua N.-H.;
 RT "The cDNA sequence of two MADS box proteins in Petunia.";
 RL Plant Physiol. 102:1051-1052(1993).
 CC -1- FUNCTION: Transcription factor involved in the genetic control of
 CC flower development.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: Predominantly expressed in petals and stamens,
 CC less in carpels and sepals.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 CC -----

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DR EMBL; X69947; CAA49568.1; ..
 DR PIR; S31707; S31707.
 DR HSSP; P11746; 1NMN.
 DR TRANSFAC; T03134.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRP-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KM Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KM Developmental protein.
 FT DOMAIN 3 58 MADS-box.
 FT DOMAIN 93 165 K-box.
 SQ SEQUENCE 212 AA; 24785 MW; FCB10C16D52E4210 CRC64;

Query Match 31.7%; Score 385; DB 1; Length 212;
 Best Local Similarity 37.9%; Pred. No. 8.3e-21;
 Matches 85; Conservative 40; Mismatches 73; Indels 26; Gaps 4;

QY 1 MARGKIEIKLLENQNRQVYTSKRNGIFPKAQLTVCDAKSLIMLNNTNKHETSP 60
 DB 1 MGRGKIEIKRIENSNRQVYTSKRNGILKKAKEITVCDKAVSLIFNGSGKHEITCSP 60
 QY 61 TTTTSMYVDYQKTMGIDLMRTHEESMDTLWKLKINNKLRREIRQRLGHDLNGSPDE 120
 DB 61 STTLPDMLDGYQKTSGRRLMDAKHENLSNEIDRIKENDNNQVRLRLHKGSIDINSLNHKE 120
 QY 121 LASLDDDEMOSSLDAIRQKRYHVIKQTETTKKKVKNLFGRGNMLHGFDEAAGE--- 176
 DB 121 LMTVEEGLTNGLSISAKQSEITLR---MVRKNQDILSEEHKQQLQYALHQEKAMAGNM 176
 QY 177 ---DPQYGEDNEGDYESALALNSGANNLYTFHLH---HPNLH 213
 DB 177 RMIEEVYHQRDYRDEYEQ-----MPPALRVQCMQGNLH 209

RESULT 6
 M3_GNEGN STANDARD; PRT; 237 AA.
 ID M3_GNEGN
 AC 09XGJ4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE MADS box protein GGM13.
 GN GGM13.
 OS Gnetum gnemon (Bago).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Gnecophyta; Gnecopsida; Gnecales; Gnecaceae; Gnetum.
 CC NCBI_TaxId=3382;
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99307411; PubMed=10377416;
 RA Winter K.-U., Becker A., Menester T., Kim J.T., Saedler H.,
 RA Theissen G.;
 RT "MADS-box genes reveal that gnecophytes are more closely related to
 RT confers than to flowering plants";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:7342-7347(1999).
 RN [2]
 RN TISSUE SPECIFICITY.
 RP MEDLINE=21851234; PubMed=11862488;
 RX Becker A., Kaufmann K., Freialdenhoven A., Vincent C., Li M.-A.,
 RA Saedler H., Theissen G.;

RT "A novel MADS-box gene subfamily with sistergroup relationship to
 RT class B floral homeotic genes";
 RL Mol. Genet. Genomics 266:942-950(2002).
 CC -1- FUNCTION: Probable transcription factor.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: Expression specific for female reproductive
 CC structures; strong at the adaxial base of the cupules, where
 CC ovules will later develop, then in the outermost cell layer of the
 CC nucellus, in the inner envelope, and in the inner half of the
 CC middle envelope at late stage of ovule development.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.

CC -1- SIMILARITY: Contains 1 MADS-box domain.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; AJ132219; CAB44459.1; ..
 DR HSSP; P11746; 1NMN.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRP-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KM Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 1 61 MADS-box.
 FT DOMAIN 69 170 K-box.
 SQ SEQUENCE 237 AA; 26943 MW; 5C65191A51D08691 CRC64;

Query Match 28.8%; Score 350.5; DB 1; Length 237;
 Best Local Similarity 36.8%; Pred. No. 2.7e-18;
 Matches 82; Conservative 45; Mismatches 85; Indels 11; Gaps 3;

QY 1 MARGKIEIKLLENQNRQVYTSKRNGIFPKAQLTVCDAKSLIMLNNTNKHETSP 60
 DB 1 MGRGKIEIKRIENSNRQVYTSKRNGILKKAKEITVCDKAVSLIFNGSGKHEITCSP 60
 QY 61 TTTTSMYVDYQKTMGIDLMRTHEESMDTLWKLKINNKLRREIRQRLGHDLNGSPDE 120
 DB 61 TTTTSMYVDYQKTMGIDLMRTHEESMDTLWKLKINNKLRREIRQRLGHDLNGSPDE 120
 QY 61 SSMKKIIEIRYQVSGARITIEYDNOHLVCEMTKMKENELQNTNIRRMGEDILSLTME 120
 DB 61 LASLDDDEMOSSLDAIRQKRYHVIKQTETTKKKVKNLFGRGNMLHGFDEAAGEPO- 179
 QY 121 LHLGQQLBSASRSVRKQQLWLOLEMLRRERITLEDONSHCLLAEQRAVGVGE 180
 DB 180 ---YGEYEDNEGDYESALALNSG---ANNTLYTFHLH---HPNL 212
 QY 181 PLIEFVFCPPDPNKTAAANAGPLHLGHLPFRLOTPQNL 223
 DB 181 PLIEFVFCPPDPNKTAAANAGPLHLGHLPFRLOTPQNL 223

RESULT 7
 GLOB_ANTMA STANDARD; PRT; 215 AA.
 ID GLOB_ANTMA
 AC Q03378;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Floral homeotic protein GLOBOSA.
 GN GLO.
 OS Antirrhinum majus (Garden snapdragon).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 CC Lamiales; Antirrhinales; Antirrhinales; Antirrhinales; Antirrhinales;
 CC NCBI_TaxId=4151;
 RN [1]
 RN SEQUENCE FROM N.A.

RX MEDLINE=93099842; PubMed=1361166;
 RA Treiber W., Ramirez L., Motte P., Hue I., Huijser P., Loening W.-E.,
 RA Siedler H., Sommer H., Schwartz-Sommer Z.,
 RT "GLOBOSA: a homeotic gene which interacts with DEFICIENS in the
 RL control of Antirrhinum floral organogenesis.";
 RL EMO J. 11:4693-4704(1992).
 CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
 CC FLOWER DEVELOPMENT. ACTS IN CONJUNCTION WITH DEFICIENS (DEFA).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- MISCELLANEOUS: MUTATIONS IN GLO CAUSE TRANSFORMATION OF PETALS
 CC INTO SEPAL AND STAMINA INTO CARPELS.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC
 DR EMBL; X68831; CAA48725.1; -
 DR PIR; S28062; S28062.
 DR HSSP; P11746; 1MM.
 DR TRANSFAC; T01778; -
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRP-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KM Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KM Developmental protein.
 FT DOMAIN 3
 FT DOMAIN 57
 SQ SEQUENCE 215 AA; 25363 MW; 0DE2A3E37815B7E4 CRC64;
 Query Match 28.6%; Score 347.5; DB 1; Length 215;
 Best Local Similarity 34.1%; Pred. No. 4e-18; Index 29; Gaps 5;
 Matches 77; Conservative 49; Mismatches 71; Indels 29; Gaps 5;
 QY 1 MARGKIEIKLIENTNQVYTSKRNGIFPKAQLVLCDAKYSILMSTNKGHEIYSP 60
 DB 1 MGRKIKIKIENSNNQVYTSKRNGIMKKAKEISVLCDAHVSIIIFASSGKMHFESP 60
 QY 61 TTTTSMYDDYQKTMGIDLWRTHEESKMDLTKLKEINNKLRRIQRGLDNLGSLFDE 120
 DB 61 STLVLDMLDHYHKLSGKRLWDPKHEHLDNEINVKKENDSMQLELHKLKEDITTLNLYE 120
 QY 121 LASLDDEMOSSLDAIRORKYHVTK-----TQTEYTKKVKVNLQRRGNMLHGY 168
 DB 121 LMLVEDALDNLGSLTKKQKMEFYAMRKHNEMTEENQSIQFLRQMHLDPMNDVNM--- 177
 QY 169 FDQFAGEDPQYGEDNEDGESALALSGANNLYTFHLH--HPNL 212
 DB 178 -ESQAYVD---HHHQNIADYEAKMP-----FAFRVQPMCPNL 211
 RESULT 8
 GLOB_TOBAC STANDARD; PRT; 209 AA.
 ID GLOB_TOBAC
 AC Q03416;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Floral homeotic protein GLOBOSA.
 GN GLO.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC lamids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=cv. Sri; TISSUE=flower;
 RX MEDLINE=93288002; PubMed=8099711;
 RA Hansen G., Estruch J.J., Sommer H., Spena A.,
 RT "NTGLO: a tobacco homologue of the GLOBOSA floral homeotic gene of
 RL Antirrhinum majus: cDNA sequence and expression pattern.";
 RL Mol. Gen. Genet. 239:310-312(1993).
 CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
 CC FLOWER DEVELOPMENT. ACTS IN CONJUNCTION WITH DEFICIENS (DEFA).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: EXPRESSED MAINLY IN FLORAL ORGANS AND, WITHIN
 CC THE FLOWER, EXPRESSION IS RESTRICTED TO PETALS AND STAMENS.
 CC -1- MISCELLANEOUS: MUTATIONS IN GLO CAUSE TRANSFORMATION OF PETALS
 CC INTO SEPAL AND STAMINA INTO CARPELS.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC
 CC
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 CC
 CC
 DR EMBL; X67959; CAA48142.1; -
 DR PIR; S35226; S35226.
 DR HSSP; P11746; 1MM.
 DR TRANSFAC; T01779; -
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRP-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KM Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KM Developmental protein.
 FT DOMAIN 3
 FT DOMAIN 57
 SQ SEQUENCE 209 AA; 24691 MW; 5661F9C1640E1A47 CRC64;
 Query Match 28.0%; Score 340.5; DB 1; Length 209;
 Best Local Similarity 34.7%; Pred. No. 1.2e-17; Index 21; Gaps 5;
 Matches 76; Conservative 49; Mismatches 73; Indels 21; Gaps 5;
 QY 1 MARGKIEIKLIENTNQVYTSKRNGIFPKAQLVLCDAKYSILMSTNKGHEIYSP 60
 DB 1 MGRKIEIKIENSNNQVYTSKRNGILKKAKEISVLCDAHVSIIIFASSGKMHFESP 59
 QY 61 TTTTSMYDDYQKTMGIDLWRTHEESKMDLTKLKEINNKLRRIQRGLDNLGSLFDE 120
 DB 61 TSLVDILDQYHKLGRRLWDKHEHLDNEINVKKENDSMQLELHKLKEDITSLNRE 118
 QY 121 LASLDDEMOSSLDAIRORKYHVTK-----TQTEYTKKVKVNLQRRGNMLHGYFDQFAGEDPQY 180
 DB 119 LMLVEDALDNLGSLTKKQKMEFYAMRKHNEMTEENQSIQFLRQMHLDPMNDVNM--- 174
 QY 181 G-----YEDNEGYESALALSGANNLYTFHLH--HPNL 212
 DB 175 GEIGEVFORENEYQTOPMP-----FAFRVQPMCPNL 205
 RESULT 9
 M17_MAIZE STANDARD; PRT; 259 AA.
 ID M17_MAIZE
 AC Q8VWM8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE MADS box protein ZMM17.
 GN M17.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 NC NCB1_Taxid=4577;
 RX MEDLINE=21851234; PubMed=11862488;
 RA Becker A., Kaufmann K., Freialdenhoven A., Vincent C., Li M.-A.,
 RA Seidler H., Theissen G.,
 RA "A novel MADS-box gene subfamily with sistergroup relationship to
 class B floral homeotic genes.";
 RL Mol. Genet. Genomics 266:942-950 (2002).
 CC -1- FUNCTION: Probable transcription factor.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: Strong expression in female inflorescences
 (ears), but also weak expression in male inflorescences (tassels).
 CC At early stages of the development of the female spikelet,
 CC expressed in all organ primordia but later restricted to the ovule
 CC and the developing silk. At very late stages of development,
 CC expression becomes restricted to parts of the silk.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: AJ271208; CAC81053.1; -
 CC InterPro: IPR002487; TF_Kbox.
 CC InterPro: IPR002100; TF_MADSbox.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADSBOX.M.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS00350; MADS_BOX_2; 1.
 DR Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 1 61 MADS-box.
 FT DOMAIN 69 171 K-Box.
 SQ SEQUENCE 259 AA; 29001 MW; B94E7F1D9420D44 CRC64;
 Query Match 27.3%; Score 332; DB 1; Length 259;
 Best Local Similarity 33.0%; Pred. No. 6.3e-17;
 Matches 87; Conservative 46; Mismatches 93; Indels 38; Gaps 9;
 QY 1 MARGKIEIKLENNQNNRQVTSKRNKGIFFKKAQELTVCPAKVSLIMKSNKKHEHYSP 60
 DB 1 MGRGKIEIKRIENSTNRQVTSKRNKGIFFKKAQELTVCPAKVSLIMKSNKKHEHYSP 60
 QY 61 TTTTSNVDYDQKTYGIDLMR-THEESMKDILMLKEINNNKREIRORLCHDNLGSLFD 119
 DB 61 ACSAREILBOYOHANSHFEEINHDQILLMTNRKNKMELENGIRYVTDLSSLLTD 120
 QY 120 ELASJDDMEQSLDAIRQKRVHVTQETTTKKKYNLEQRGNMLHGYF--DQEA-- 174
 DB 121 DVSDLEQQLSEYSSVKRARKQQLNQQLDNRRKQILL--QNTFLYMINENQQAALTG 179
 QY 175 -----GE-----DPQYEDNEGDYESALALSNQANLTY-----FHLD- 208
 DB 180 EYKLGEMAPLAWLCPPPAFAHGATAYVGGSSSSG--TALQLMSAAPQLHADDGFRLOP 237
 QY 209 -HPNTHGGSSSLGSSITLHLRL 231
 DB 238 TQPNLQDPPAPCGG--LHGHIQL 259

RESULT 10
 ID PIST ARATH STANDARD; PRT; 208 AA.
 AC P48007; Q9SQ007; Q9SQ008; Q9SQ009; Q9SQ010; Q9SQ011; Q9SQ012; Q9SQ013;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Floral homeotic protein PISTILLATA (Transcription factor PI).
 GN PI OR AT5G20240 OR F5024.130.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 NC NCB1_Taxid=3702;
 RX MEDLINE=95047314; PubMed=7956839;
 RA Goto K., Meyerowitz E.M.;
 RA "Function and regulation of the Arabidopsis floral homeotic gene
 PISTILLATA.";
 RL Genes Dev. 8:1548-1560 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Landsberg erecta;
 RX MEDLINE=20233824; PubMed=10769227;
 RA Homma T., Goto K.;
 RA "The Arabidopsis floral homeotic gene PISTILLATA is regulated by
 RT discrete cis-elements responsive to induction and maintenance
 RT signals.";
 RL Development 127:2021-2030 (2000).
 RN [3]
 RP SEQUENCE FROM N.A. AND VARIANTS.
 RC STRAIN=cv. Bla-1, cv. Breteagny, cv. Bs-1, cv. Bu-0, cv. Bu-2,
 RC cv. Chi-1, cv. Co-1, cv. Columbia, cv. Corsacalla-1, cv. Cv1-0,
 RC cv. Gr-3, cv. J1-1, cv. Kas-1, cv. Kent, cv. Landsberg erecta,
 RC cv. Li-3, cv. Li-8, and cv. Lisse;
 RX MEDLINE=99126449; PubMed=9927474;
 RA Purgsanan M.D., Sudlith J.I.;
 RA "Molecular population genetics of floral homeotic loci: departures
 RT from the equilibrium-neutral model at the APETALA3 and PISTILLATA
 RT genes of Arabidopsis thaliana.";
 RL Genetics 151:839-848 (1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016721; PubMed=1130714;
 RA Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E.,
 RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
 RA Kohara M., Matsumoto M., Matsumoto A., Muraki A., Nakayama S.,
 RA Nakazaki N., Naruo K., Okumura S., Shino S., Takeuchi C., Wada T.,
 RA Matsuda E., Yamada K., Yasuda M., Sato S., de la Bastide M.,
 RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
 RA Haberman K., Murray J., Johnson D., Kohling T., Nelson J.,
 RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
 RA Belter E., Cordum H., Cordes M., Courtney L., Courtney C., Dante M.,
 RA Du H., Edwards J., Fryman J., Haakensen B., Lamer E., Latreille P.,
 RA Leonard S., Meyer K., Mullaney E., Ozersky P., Riley A., Stromatt C.,
 RA Wagner-McPherson C., Wollam A., Yeakum M., Ball M., Dedhia N.,
 RA Parnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,
 RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.A.,
 RA Martensen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
 RA Volckert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,
 RA Ertan K.-D., Terry N., Hartley N., Bent E., Johnson S.,
 RA Langham S.-A., McCullagh B., Robben J., Glynnoprez B., Zimmermann W.,
 RA Ramsperger U., Wedler K., Balke K., Wedler E., Peters S.,
 RA van Staveren M., Dirke W., Moollman P., Klein lankhorst R.,
 RA Weitzneger T., Bothe G., Rose W., Hauf J., Benelaiser S., Hempel S.,
 RA Feldpausch M., Lamberth S., Villarroel R., Gelen J., Ardiles W.,
 RA Bente O., Lemcke K., Kolesov G., Mayer K.F.X., Rued S., Schoof H.,
 RA Schneller C., Zaccaria P., Mewes H.-W., Bevan M., Franz P.F.;

"Sequence and analysis of chromosome 5 of the plant Arabidopsis thaliana." Nature 408:823-826(2000).

[5]

FUNCTION.

MDLINE=96152196; PubMed=8565821;

Kritzeck B.A., Meyerowitz E.M.;

"The Arabidopsis homeotic genes APETALA3 and PISTILLATA are sufficient to provide the B class organ identity function." Development 122:11-22(1996).

[6]

CHARACTERIZATION.

MDLINE=96209811; PubMed=8643482;

Riechmann J.L., Kritzeck B.A., Meyerowitz E.M.;

"Dimerization specificity of Arabidopsis MADS domain homeotic proteins APETALA1, APETALA3, PISTILLATA, and AGAMOUS." Proc. Natl. Acad. Sci. U.S.A. 93:4793-4798(1996).

[7]

GENETIC REGULATION.

MDLINE=21178805; PubMed=11283333;

Ng M., Yanofsky M.F.;

"Activation of the Arabidopsis B class homeotic genes by APETALA1." Plant Cell 13:739-753(2001).

[8]

CHARACTERIZATION.

MDLINE=21074934; PubMed=11206550;

Homma T., Goto K.;

"Complexes of MADS-box proteins are sufficient to convert leaves into floral organs." Nature 409:525-529(2001).

-1- FUNCTION: Probable transcription factor involved in the genetic control of flower development. Is required for normal development of petals and stamens in the wild-type flower. Forms an heterodimer with APETALA3 that is required for autoregulation of both AP3 and PI genes. AP3/PI heterodimer interacts with APETALA1 or SEPALLATA3 to form a ternary complex that could be responsible for the regulation of the genes involved in the flower development.

-1- SUBUNIT: Forms an heterodimer with APETALA3, capable of binding to CArG-box sequences. AP3/PI heterodimer binds AP1 or SEP3 to form a ternary complex.

-1- SUBCELLULAR LOCATION: Nuclear.

-1- INDUCTION: Positively regulated by the meristem identity proteins APETALA1 and LAFY with the cooperation of UFO.

-1- MISCELLANEOUS: Mutations in PI cause transformation of petals into sepals and stamens into carpels.

-1- SIMILARITY: Contains 1 MADS-box domain.

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EMBL; D30807; BA06465.1; -

EMBL; AB035137; BA067000.1; -

EMBL; AF115815; AAD51984.1; -

EMBL; AF115816; AAD51985.1; -

EMBL; AF115817; AAD51986.1; -

EMBL; AF115818; AAD51987.1; -

EMBL; AF115819; AAD51988.1; -

EMBL; AF115820; AAD51989.1; -

EMBL; AF115821; AAD51990.1; -

EMBL; AF115822; AAD51991.1; -

EMBL; AF115823; AAD51992.1; -

EMBL; AF115824; AAD51993.1; -

EMBL; AF115825; AAD51994.1; -

EMBL; AF115826; AAD51995.1; -

EMBL; AF115827; AAD51996.1; -

EMBL; AF115828; AAD51997.1; -

EMBL; AF115829; AAD51998.1; -

EMBL; AF115830; AAD51999.1; -

EMBL; AF296825; -; NOT_ANNOTATED_CDS.

PIR; AS3839; AS3839.

HSP; P11746; INNM.

TRANSFAC; T03129; -

InterPro; IPR002487; TF_Kbox.

InterPro; IPR002100; TF_MADSbox.

Pfam; PF01486; K-box; 1.

Pfam; PF00319; SRF-TF; 1.

PRINTS; PR00404; MADSDOMAIN.

SMART; SM00432; MADS; 1.

PROSITE; PS00350; MADS_BOX_1; 1.

PROSITE; PS00066; MADS_BOX_2; 1.

Flowering; Transcription regulation; Activator; Developmental protein; Nuclear protein; DNA-binding; Coiled coil; Polymorphism.

MDLINE=21074934; PubMed=11206550;

Homma T., Goto K.;

"Complexes of MADS-box proteins are sufficient to convert leaves into floral organs." Nature 409:525-529(2001).

-1- FUNCTION: Probable transcription factor involved in the genetic control of flower development. Is required for normal development of petals and stamens in the wild-type flower. Forms an heterodimer with APETALA3 that is required for autoregulation of both AP3 and PI genes. AP3/PI heterodimer interacts with APETALA1 or SEPALLATA3 to form a ternary complex that could be responsible for the regulation of the genes involved in the flower development.

-1- SUBUNIT: Forms an heterodimer with APETALA3, capable of binding to CArG-box sequences. AP3/PI heterodimer binds AP1 or SEP3 to form a ternary complex.

-1- SUBCELLULAR LOCATION: Nuclear.

-1- INDUCTION: Positively regulated by the meristem identity proteins APETALA1 and LAFY with the cooperation of UFO.

-1- MISCELLANEOUS: Mutations in PI cause transformation of petals into sepals and stamens into carpels.

-1- SIMILARITY: Contains 1 MADS-box domain.

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EMBL; D30807; BA06465.1; -

EMBL; AB035137; BA067000.1; -

EMBL; AF115815; AAD51984.1; -

EMBL; AF115816; AAD51985.1; -

EMBL; AF115817; AAD51986.1; -

EMBL; AF115818; AAD51987.1; -

EMBL; AF115819; AAD51988.1; -

EMBL; AF115820; AAD51989.1; -

EMBL; AF115821; AAD51990.1; -

EMBL; AF115822; AAD51991.1; -

EMBL; AF115823; AAD51992.1; -

EMBL; AF115824; AAD51993.1; -

EMBL; AF115825; AAD51994.1; -

EMBL; AF115826; AAD51995.1; -

EMBL; AF115827; AAD51996.1; -

EMBL; AF115828; AAD51997.1; -

RT mutant petunia flowers.";
 RL Plant Cell 4:983-993(1992).
 CC -1- FUNCTION: Probable transcription factor.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: PETAL.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
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 CC -----
 DR EMBL, M91190; AAA3731.1; -
 DR PIR, J01689; J01689.
 DR HSP, F11746; ILMN.
 DR TRANSFAC; T03092; -
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR Transcription regulation; DNA-binding; Nuclear protein.
 KW DOMAIN 3 57 MADS-box.
 FT DOMAIN 91 163 K-BOX.
 SQ SEQUENCE 210 AA; 24647 MW; B2D3718BE6A157C8E CRC64;
 Query Match 26.8%; Score 326; DB 1; Length 210;
 Best Local Similarity 40.9%; Pred. No. 1.3e-16;
 Matches 67; Conservative 41; Mismatches 50; Indels 6; Gaps 2;
 QY 1 MARGIEIKLTENQNNPOTVTSKRNNGIFKRAQELTVCDKAVSLMSTNNKHHEVSP 60
 DB 1 MGRGIEIKLTENQNNPOTVTSKRNNGIFKRAQELTVCDKAVSLMSTNNKHHEVSP 59
 QY 61 TTTKSMVDYQKTMGIDIMRTHEESMDTKLKEINNKRLREIQRIGDLNGLSPDE 120
 DB 60 -TSIVDILIDQYHKLGRRLDLAKHNDLNEINKVKKDNDQIELRHKGEDILSNRE 118
 QY 121 LASLDDMOSSLDARQKTHVTKQTETTKKKVKNLEQRGNM 164
 DB 119 LMLIEDALENGLTSIRNKQNEVLRW---RKKTQSMEEBDQL 158
 RESULT 12
 TT16 ARATH STANDARD; PRT; 252 AA.
 ID TT16 ARATH
 AC Q8RYD9; Q8RYD9; 41; Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE TRANSPARENT TESTA 16 protein (Arabidopsis BISISTER MADS box protein).
 GN TT16 OR ABS OR AT5G23260 OR MD15.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eustersid II; Brassicales; Brassicaceae; Arabidopsis.
 CC [1]
 RN [1]
 RP SEQUENCE FROM N.A. (TSCOROM 1).
 RC STRAIN=cv. Columbia; TISSUE=green siliques;
 RX MEDLINE=21951234; PubMed=11862488;
 RA Becker A., Kaufmann K., Fretaldenhoven A., Vincent C., Li M.-A.,
 RA Saedler H., Theissen G.,
 RT "A novel MADS-box gene subfamily with sistergroup relationship to
 RT class B floral homeotic genes";
 RL Mol. Genet. Genomics 266:942-950(2002).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98162728; PubMed=9501997;
 RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
 RA Tabata S.,
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
 RT Sequence features of the regions of 1,191,918 bp covered by seventeen
 RT physically assigned P1 clones";
 RL DNA Res. 4:401-414(1997).
 RN [3]
 RP CHARACTERIZATION, AND ALTERNATIVE SPLICING.
 RX MEDLINE=2226155; PubMed=12368498;
 RA Nesi N., Debeaujon I., Jond C., Stewart A.J., Jenkins G.I.,
 RA Caboche M., Lepointec L.,
 RT "The TRANSPARENT TESTA16 locus encodes the ARABIDOPSIS BISISTER MADS
 RT domain protein and is required for proper development and
 RT pigmentation of the seed coat."
 RL Plant Cell 14:2463-2479(2002).
 CC -1- FUNCTION: Transcription factor involved in the developmental
 CC regulation of the endodermis and in the accumulation of
 CC proanthocyanidins (PAs) or condensed tannins which give the seed
 CC its brown pigmentation after oxidation. Necessary for the normal
 CC activation of the BANYUS promoter in the endodermis body.
 CC -1- PATHWAY: Flavonoid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC IsoId=Q8RYD9-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8RYD9-2; Sequence=VSP_006257;
 CC -1- TISSUE SPECIFICITY: Expressed in buds, flowers and immature seeds,
 CC but not in roots, stems, leaves, seedlings or siliques valves.
 CC Expression in seed coat is confined to the endodermis layer.
 CC -1- DEVELOPMENTAL STAGE: Expressed during seed development.
 CC -1- MISCELLANEOUS: The two isoforms were always coexpressed in the
 CC tissues investigated. The pigmentation of the chalazal-microphyte
 CC region is not under the control of ABS, as opposed to the
 CC pigmentation of the seed body.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC -----
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 CC -----
 DR EMBL, AJ318098; CAC85664.1; -
 DR EMBL, AB007648; BAB1181.1; ALT_SEQ.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW Flavonoid biosynthesis; Transcription; Transcription regulation;
 KW DNA-binding; Alternative splicing; Nuclear protein; Coiled coil.
 FT DOMAIN 1 61 MADS-box.
 FT DOMAIN 73 172 K-BOX.
 FT DOMAIN 121 174 COILED COIL (POTENTIAL).
 FT DOMAIN 180 222 GIN-RICH.
 FT VARSPLIC 142 146 Missing (1n isoform 2).
 FT SEQUENCE 252 AA; 29697 MW; 2C4ECB9D9CIDEA8 CRC64;
 /FTID=VSP_006257.

Query Match 26.4%; Score 320.5; DB 1; Length 252;
 Best Local Similarity 32.7%; Pred. No. 4e-16;
 Matches 80; Conservative 39; Mismatches 95; Indels 31; Gaps 3;

QY 1 MARGKIEIKLENTNQNTVTSKRRNGIFPKAQLTYLCAKXSLIMLSTNNKHEVISP 60
 1 MGRKIEIKLENTNQNTVTSKRRNGIFPKAQLTYLCAKXSLIMLSTNNKHEVISP 60
 DB 1 MGRKIEIKLENTNQNTVTSKRRNGIFPKAQLTYLCAKXSLIMLSTNNKHEVISP 60
 QY 61 TTTKSMYDDYQKTMGIDLWRTN--EESMKTLMKLEINNKLRREIRQLGHDLGSLF 118
 61 QNRMPQIDRYLHNGRLPDPHDDQQLHEHMEELRFETCNLELRPFPHGDLASIPP 120
 DB 119 DELASLIDEMQSSLDALRQRKYHVIKTQETTTKKVKNLEQRGNMHLGFFDDEAGDEP 178
 121 NELDGLERQLEHSLVLYKVRERKNELMQOOLENLSKRRMLEEDNNNIRMLHEHRAAMEPQ 180
 QY 179 QYGYEDNEGVE-----SALALSGANNL--YTFELH 209
 181 QAGIDTRPGEVQCFEQLQCKPGEYQGFLEQQQQQNSVLQATLPSEIDPTYNQLAQ 240
 DB 210 PNLH 214
 241 PNLON 245

RESULT 13
 FB24_PETHY STANDARD; PRT; 268 AA.

ID FB24_PETHY STANDARD; PRT; 268 AA.
 AC Q9ATE5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE MADS box protein FB24 (Floral binding protein 24).
 GN FB24.
 OS Petunia hybrida (Petunia).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Petunia.
 OC NCBI_TaxID=4102;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. M15;
 RA Ferrario S., Buescher-Lange J., Buescher M., Argente G.;
 RT "Petunia hybrida MADS-box transcription factor FB24."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBD databases.
 CC -1- FUNCTION: Probable transcription factor.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-4 is the initiator.
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 CC -----
 CC EMBL; AF35242; AAK21255.1; -
 DR HSBP; P11831; ISRS.
 DR InterPro: IPR002487; TF_Kbox.
 DR InterPro: IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSOMAIN.
 DR SMART; SMO0432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS00350; MADS_BOX_2; 1.
 KM Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 4 64 MADS-box.
 FT DOMAIN 72 174 K-box.
 FT DOMAIN 187 196 HIS-RICH.

SQ SEQUENCE 268 AA; 31119 MW; 4C854DB87F36F16A CRC64;
 Query Match 25.2%; Score 307; DB 1; Length 268;
 Best Local Similarity 31.6%; Pred. No. 3.9e-15;
 Matches 83; Conservative 44; Mismatches 90; Indels 46; Gaps 6;

QY 1 MARGKIEIKLENTNQNTVTSKRRNGIFPKAQLTYLCAKXSLIMLSTNNKHEVISP 60
 1 MGRKIEIKLENTNQNTVTSKRRNGIFPKAQLTYLCAKXSLIMLSTNNKHEVISP 60
 DB 4 MGRKIEIKLENTNQNTVTSKRRNGIFPKAQLTYLCAKXSLIMLSTNNKHEVISP 60
 QY 61 TTTKSMYDDYQKTMGIDLWRTN--EESMKTLMKLEINNKLRREIRQLGHDLGSLF 119
 64 PHSMQIISRLQTTGASLPEDNRVQLYDEVAQRDITNLQLQRYKGDLSLQYE 123
 DB 120 ELASLIDEMQSSLDALRQRKYHVIKTQETTTKKVKNLEQRGNMHLGFFDDEAG 174
 124 ELNELKQLEHSLVLYKVRERKNELMQOOLENLSKRRMLEEDNNNIRMLHEHRAAMEPQ 183
 QY 175 -----GEDPQYGYEDNEGVE-----SALALSGANNL--YTFELH 209
 184 AMDHEDHHHHHROQALTEALNLEQPLSHFTFGQEQPSTSTVNHFAISILSPAN 243
 DB 201 NLTYFHLH--HPNLH---HGGS 217
 244 SISPYRLQPSHPNLQDSHVHGGS 266

RESULT 14
 DE21_ANTMA STANDARD; PRT; 247 AA.

ID DE21_ANTMA STANDARD; PRT; 247 AA.
 AC Q8RYL4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE MADS box protein dehn21 (DEFICIENS homolog 21).
 GN DEHN21.
 OS Antirrhinum majus (Garden snapdragon).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Antirrhineae; Antirrhineae; Antirrhinum.
 OC NCBI_TaxID=4151;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=flower buds;
 RX MEDLINE=21851234; PubMed=11862488;
 RA Becker A., Kaufmann K., Freialdenhoven A., Vincent C., Li M.A.,
 Saedler H., Theissen G.;
 RT "A novel MADS-box gene, subfamily with sistergroup relationship to
 class B floral homeotic genes."
 RL Mol. Genet. Genomics 266:942-950(2002).
 CC -1- FUNCTION: Probable transcription factor.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: Expressed exclusively in a few inner cell
 CC layers of the inner integuments of the ovules.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
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 CC -----
 CC EMBL; AJ307056; CAC85225.1; -
 DR InterPro: IPR002487; TF_Kbox.
 DR InterPro: IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSOMAIN.
 DR SMART; SMO0432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.

DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 1 61 MADS-box.
 FT DOMAIN 74 177 K-BOX.
 SQ SEQUENCE 247 AA; 29052 MW; 7BDF23BC7C504371 CRC64;
 Query Match 24.5%; Score 297.5; DB 1; Length 247;
 Best Local Similarity 37.9%; Pred. No. 1.7e-14;
 Matches 66; Conservative 35; Mismatches 64; Indels 9; Gaps 2;
 Oy 1 MARGKIEIKLIENTQNRQVTSKRRNGIFKKAQELTVLCAKVSILMLSNTKMHEYISP 60
 1 MGRGKIEIKRLENTSRQVTSKRRSGILMKTHLSVLCDAQILYFSTGKLTCTP 60
 Db 1 TTTTSMYDDYQXTWGI-----DLWRTHESSKDTLWKLEINNKLRREIRQLGHD 112
 Oy 61 PPSMKQIIDRYVYKAGIIPENENRAGPHADNDQVYKE-LTRMKEETLNLQNLQRYKGGD 119
 Db 113 LNSGSPDELASLDDEMOSSLDAIRQKRYHVIKTQETTKKKVKKLEORGMHL 166
 120 LSTVRFELTELEKLDQSLMKVRAKLELHGEVKNLKRTEPMLEKENQEMTH 173
 RESULT 15
 AG14_ARATH STANDARD; PRT; 221 AA.
 ID AG14_ARATH Q97056;
 AC Q36838; Q97056;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Agamox-like MADS box protein AG14.
 GN AG14 OR AT4G11880 OR T26M18.90.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid 11; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Scheller C., Wandura R., Murphy G., Volckaert G.,
 Pohl T., Duesterhoef A., Stiekema W., Entlan K.-D., Terryn N.,
 Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
 Weichselgartner M., de Simone V., Obermayer B., Macho R., Meier M.,
 Kreis M., Delseny M., Pidgomech P., Watson M., Schmidheini T.,
 Reichert B., Portetle D., Perez-Alonso M., Boutry M., Bancroft I.,
 Vos P., Hohenseil J., Zimmermann W., Wedler H., Ridley P.,
 Langham S.-A., McCullagh B., Biham L., Roben J.,
 Van der Schueren J., Grymptre B., Chuang Y.-D., Vandenbussche F.,
 Brecken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 Weltzenger T., Bohe G., Rameberger U., Hilbert H., Braun M.,
 Holzner E., Brandt A., Peters S., van Staveren M., Dikse W.,
 Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koester P.,
 Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 de Keyser A., Buysaert C., Gielen J., Villarroel R., De Clercq R.,
 Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen E.,
 Clark L., Doggett J., Hall S., Kay M., Leonard N., Molay K., Mayes R.,
 Portet A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 Borova D., Bloeker H., Scharfe M., Grimm M., Lochner T.-H.,
 Dore S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 Gabel C., Fuchs M., Fattmann B., Granderath K., Danner D., Herzl A.,
 Neumann S., Aguilou A., Vitale D., Uguori R., Piravandi E.,
 Maeser O., Guilely F., Clabaud G., Wundt A., Felber R.,
 Schnabl S., Hiller R., Berger C., Montfort A., Casacuberta E.,
 Ghibons T., Weber N., Schmidt W., Lecharny A., Aubourg S.,
 Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bieler C.,
 Frithman D., Haase D., Lemcke K., Wewes H.-M., Stocker S.,
 Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 Parrell L., Dedha N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,

RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Clout J., Abbott A., Scott K., Johnson D.,
 RA Manx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hiller L.W.,
 RA Nelson J., Splich J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Dron K., Cotton M., Joshi C.,
 RA Antonin B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Val D., Shekier M., Matero A., Shah R.,
 RA Saby I.K., O'Shaughnessy A., Rodriguez W., Hoffman J., Hill S.,
 RA Grant S., Shohdy N., Hasegawa A., Hamed A., Lohd M., Johnson A.,
 RA Chen E., Marra M.A., Martienssen R., McCombie W.R.,
 RA "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana."
 RT thaliana.
 RL Nature 402:769-777(1999).
 RN [2]
 RP SEQUENCE OF 7-221 FROM N.A.
 RC STRAIN=cv. Landsberg erecta; TISSUE=Root;
 RX MEDLINE=96004530; PubMed=7549482;
 RA Rounleay S.D., Ditta G.S., Yanofsky M.F.,
 RT "Diverse roles for MADS box genes in Arabidopsis development."
 RL Plant Cell 7:1259-1269(1995).
 CC -1- FUNCTION: Probable transcription factor.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: Preferentially expressed in roots.
 CC -1- SIMILARITY: Contains 1 K-box dimerization domain.
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
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 CC -----
 DR EMBL; AL078606; CAB44526.1; -;
 DR EMBL; AL161532; CAB78231.1; -;
 DR EMBL; U20184; AAC49082.1; -;
 DR PIR; T09347; T09347.
 DR HSSP; P11746; 1MNM.
 DR TRANSFAC; T03012; -;
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box_1.
 DR Pfam; PF00319; SRP-TP_1.
 DR PRINTS; PR00404; MADSBOXMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3 57 MADS-box.
 FT DOMAIN 96 168 K-BOX.
 FT CONFLICT 103 103 H -> D (IN REF. 2).
 FT CONFLICT 187 188 ST -> TS (IN REF. 2).
 FT CONFLICT 188 188 ST -> TS (IN REF. 2).
 SQ SEQUENCE 221 AA; 25492 MW; E876DAEA049B125E CRC64;
 Query Match 24.4%; Score 296.5; DB 1; Length 221;
 Best Local Similarity 41.4%; Pred. No. 1.8e-14;
 Matches 67; Conservative 35; Mismatches 53; Indels 7; Gaps 3;
 Oy 1 MARGKIEIKLIENTQNRQVTSKRRNGIFKKAQELTVLCAKVSILMLSNTKMHEYISP 60
 1 MGRGKIEIKRLENTSRQVTSKRRSGILMKTHLSVLCDAQILYFSTGKLTCTP 60
 Db 1 TTTTSMYDDYQXTWGI-----ESMKDTLWKLEINNKLRREIRQLGHD 115
 Oy 61 PPSMKQIIDRYVYKAGIIPENENRAGPHADNDQVYKE-LTRMKEETLNLQNLQRYKGGD 119
 Db 116 LNSGSPDELASLDDEMOSSLDAIRQKRYHVIKTQETTKKKVKKLEORGMHL 157
 119 LSTVRFELTELEKLDQSLMKVRAKLELHGEVKNLKRTEPMLEKENQEMTH 160

Search completed: September 27, 2004, 09:25:46
Job time : 17.5705 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 27, 2004, 09:18:34 / Search time 74.7383 Seconds
(without alignments)
979.421 Million cell updates/sec

Title: US-10-069-527-4
Sequence: 1216
1 MARGKLEIKLENTQNRQVT.....HGGSSLGSSITHLHLRLA 232

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mbc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriopl:*
- 17: sp_archaeopl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1203	98.9	232	10	Q8VWZ4
2	1072.5	88.2	237	10	Q8L5M8
3	882.5	72.6	261	10	Q93X10
4	721.5	59.3	225	10	Q91LAI
5	709.5	58.3	226	10	Q9ZS28
6	709.5	58.3	227	10	Q65211
7	690.5	56.8	222	10	Q40171
8	690.5	56.8	222	10	Q8H282
9	682	56.1	238	10	Q84U28
10	659	58.2	201	10	Q91LA2
11	638	55.5	227	10	Q40513
12	628.5	51.7	228	10	Q41417
13	624.5	51.4	228	10	Q41417
14	623.5	51.3	247	10	Q40352
15	623	51.2	228	10	Q65141
16	620.5	51.0	229	10	Q49173

17	616	50.7	228	10	Q8L710	Q8L710 illium rega
18	612	50.3	228	10	Q8LRS9	Q8LRS9 illium long
19	612	50.3	229	10	Q7X918	Q7X918 rosa rugosa
20	600.5	49.4	221	10	Q9FR12	Q9FR12 hemerocalli
21	597	49.1	228	10	Q84M22	Q84M22 tulipa gesn
22	595	48.9	214	10	Q948U8	Q948U8 magnolia pr
23	590.5	48.6	225	10	Q84M23	Q84M23 asparagus o
24	577	47.5	231	10	Q84M21	Q84M21 tulipa gesn
25	576	47.4	224	10	Q9SPB7	Q9SPB7 hieracium p
26	575	47.3	210	10	Q7X9P5	Q7X9P5 silene laci
27	572.5	47.1	232	10	Q96357	Q96357 brassica ol
28	569.5	46.8	202	10	Q65136	Q65136 syringa vul
29	569	46.8	210	10	Q841C1	Q841C1 helianthus
30	569	46.8	210	10	Q7X9P3	Q7X9P3 silene diol
31	569	46.8	210	10	Q7X9P1	Q7X9P1 silene diol
32	566	46.5	199	10	Q65142	Q65142 dicentra ex
33	566	46.5	228	10	Q9SPB6	Q9SPB6 hieracium p
34	563	46.3	228	10	Q9ZS27	Q9ZS27 gerbera hyb
35	562	46.2	227	10	Q41354	Q41354 silene laci
36	562	46.2	229	10	Q841D0	Q841D0 chrysanthem
37	561.5	46.2	232	10	Q841C7	Q841C7 chrysanthem
38	561	46.1	199	10	Q84Y44	Q84Y44 platanus oc
39	560.5	46.1	224	10	Q9M7M0	Q9M7M0 brassica na
40	560	46.1	210	10	Q7X9P0	Q7X9P0 silene diol
41	558.5	45.9	224	10	Q96358	Q96358 brassica ol
42	558.5	45.9	224	10	Q7XBE7	Q7XBE7 brassica na
43	557	45.8	210	10	Q7X9P4	Q7X9P4 silene laci
44	556.5	45.8	223	10	Q8L5F5	Q8L5F5 daucus caro
45	556.5	45.8	229	10	Q82130	Q82130 tritilium ae

ALIGNMENTS

RESULT 1

Q8VWZ4 PRELIMINARY; PRT; 232 AA.

Q8VWZ4;
01-MAR-2002 (T-EMBLrel.. 20, Created)
01-MAR-2002 (T-EMBLrel.. 20, Last sequence update)
01-JUN-2003 (T-EMBLrel.. 24, Last annotation update)
B-type MADS box protein.
MADS13.
Malus domestica (Apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eurosid I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vegetative growing point;
RA van der Linden C.G.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Vegetative growing point;
RA Vosman B., Smulders M.J.M.;
RT "Isolation of apple B- and C-type MADS box genes from vegetative tissue."
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AJ251116; CAC08056.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006350; P:regulation of transcription; IEA.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRP-TF; 1.
DR PRINTS; PR00404; MADSOMAIN.

DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 232 AA; 26898 MW; 73C08DA605540F9C CRC64;

Query Match 98.9%; Score 1203; DB 10; Length 232;
 Best Local Similarity 99.1%; Pred. No. 5.8e-86;
 Matches 230; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARGIKIKIENQTNQVYTSKRNGIFPKAQLTVLCPAKYSLMNSTNKHETISP 60
 DB 1 MGRKIKIKIENQTNQVYTSKRNGIFPKAQLTVLCPAKYSLMNSTNKHETISP 60
 QY 61 TTTTSMYDDYQKTMGIDLWRTHEESKMDTLMKLEINNKLRRIQRQLGHDINGLSFDE 120
 DB 61 TTTTSMYDDYQKTMGIDLWRTHEESKMDTLMKLEINNKLRRIQRQLGHDINGLSFDE 120
 QY 121 LASLDEMOSSLDLRQKRYVITQTETTTKKYKKNLEORGNMLGYPQDEAAGDPQY 180
 DB 121 LASLDEMOSSLDLRQKRYVITQTETTTKKYKKNLEORGNMLGYPQDEAAGDPQY 180
 QY 181 GYEDNEGDEYSALALSNGANNTYTFHLHPNLHHGSSLSGSSITHLHDLRLA 232
 DB 181 GYEDNEGDEYSALALSNGANNTYTFHLHPNLHHGSSLSGSSITHLHDLRLA 232

RESULT 2

QBLSM8 PRELIMINARY; PRT; 237 AA.

ID QBLSM8
 AC QBLSM8
 DT 01-OCT-2002 (TREMREL. 22, Created)
 DT 01-OCT-2002 (TREMREL. 22, Last sequence update)
 DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
 DE MADS-box protein.
 GN MDTM6.
 OS Malus domestica (Apple) (Malus sylvestris).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid 1; Rosales; Rosaceae; Maloideae; Malus.
 OC NCBI_TaxID=3750;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Indo; TISSUE=young floral parts;
 RA Matsumoto S., Ohtsubo T., Soejima Y.,
 RT "Cloning and sequencing of apple MADS-box genes 'MdPI', 'MDTM6', and
 RT 'MdMDS13'."
 CC Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL; AB081093; BAC11907.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 237 AA; 27693 MW; 71A2B357202FCF20 CRC64;

Query Match 88.2%; Score 1072.5; DB 10; Length 237;
 Best Local Similarity 87.9%; Pred. No. 8.8e-76;
 Matches 211; Conservative 9; Mismatches 9; Indels 11; Gaps 3;
 QY 1 MARGIKIKIENQTNQVYTSKRNGIFPKAQLTVLCPAKYSLMNSTNKHETISP 60

DB 1 MGRKIKIKIENQTNQVYTSKRNGIFPKAQLTVLCPAKYSLMNSTNKHETISP 60
 QY 61 TTTTSMYDDYQKTMGIDLWRTHEESKMDTLMKLEINNKLRRIQRQLGHDINGLSFDE 120
 DB 61 TTTTSMYDDYQKTMGIDLWRTHEESKMDTLMKLEINNKLRRIQRQLGHDINGLSFDE 120
 QY 121 LASLDEMOSSLDLRQKRYVITQTETTTKKYKKNLEORGNMLGYPQDEAAGDPQY 180
 DB 121 LASLDEMOSSLDLRQKRYVITQTETTTKKYKKNLEORGNMLGYPQDEAAGDPQY 180
 QY 181 GYEDNEGDEYSALALSNGANNTYTFHLHPNLHHGSSLSGSSITHLHDLRLA 232
 DB 181 GYEDNEGDEYSALALSNGANNTYTFHLHPNLHHGSSLSGSSITHLHDLRLA 232

RESULT 3

ID Q93X10 PRELIMINARY; PRT; 261 AA.

AC Q93X10
 DT 01-DEC-2001 (TREMREL. 19, Created)
 DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
 DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
 DE MADS-box protein.
 GN MASAKO B3.
 OS Rosa rugosa (Rugosa rose).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid 1; Rosales; Rosaceae; Rosoideae; Rosa.
 OC NCBI_TaxID=74645;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Young floral parts;
 RA Matsumoto S., Hirai S., Kitahara K.;
 RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Young floral parts;
 RA Kitahara K., Hirai S., Fukui H., Matsumoto S.;
 RT "Rose MADS-box genes 'MASAKO BP and B3' homologous to class B floral
 RT identity genes."
 RT Plant Sci. 161:549-557(2001).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL; AB055966; BAB63261.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 261 AA; 29777 MW; 6EBD1283977E05E CRC64;

Query Match 72.6%; Score 882.5; DB 10; Length 261;
 Best Local Similarity 66.2%; Pred. No. 6.5e-61;
 Matches 174; Conservative 24; Mismatches 32; Indels 33; Gaps 3;

QY 1 MARGIKIKIENQTNQVYTSKRNGIFPKAQLTVLCPAKYSLMNSTNKHETISP 60
 DB 1 MGRKIKIKIENQTNQVYTSKRNGIFPKAQLTVLCPAKYSLMNSTNKHETISP 60
 QY 61 TTTTSMYDDYQKTMGIDLWRTHEESKMDTLMKLEINNKLRRIQRQLGHDINGLSFDE 120
 DB 61 TTTTSMYDDYQKTMGIDLWRTHEESKMDTLMKLEINNKLRRIQRQLGHDINGLSFDE 120
 QY 121 LASLDEMOSSLDLRQKRYVITQTETTTKKYKKNLEORGNMLGYPQDEAAGDPQY 180

Db 121 LQDLEMTSGSVQIIRDKRYHVLKQATTTKRYKVNLEERSNLMHG--GAPGNDPQY 178
 QY 181 GYEDNEGDYESALALNSGANNLYTF-----HLHPVHL----- 213
 Db 179 GYVNEGDYESVALANGASNLTFPNRVHNNHLDHGGGSLVSYTLHONPNHGNH 236
 QY 214 ----HGSSLSGSIITLHDLRLA 232
 Db 239 LENGHGGSLSISITLHDLRLA 261

RESULT 4

Q9L1A1 PRELIMINARY; PRT; 225 AA.
 AC Q9L1A1: PRELIMINARY; PRT; 225 AA.
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE MADS box transcription factor TM6.
 OS Petunia hybrida (Petunia).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Petunia.
 CC NCBI_TaxID=4102;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kramer E.M., Irish V.F.;
 RT "Evolution of the petal and stamen developmental programs: Evidence from comparative studies of the lower eudicots and basal angiosperms."
 RT Int. J. Plant Sci. 0:0-0(2000).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
 DR EMBL; AF230704; AAF73933.1; -.
 DR HSP; P11746; IMNM.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRP-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS00066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 KM SEQUENCE 225 AA; 26047 MW; 765515B384C4C5DD CRC64;

Query Match 59.3%; Score 721.5; DB 10; Length 225;
 Best Local Similarity 60.7%; Pred. No. 1.9e-48;
 Matches 142; Conservative 32; Mismatches 49; Indels 11; Gaps 4;

QY 1 MARGKIEIKLIENTRQVYTSKRNGIFPKAQELTVLCAKYSILMLSTNNMHEIYSP 60
 Db 1 MARGKIEIKLIENTRQVYTSKRNGIFPKAKELTVLCAKICILMLSTRKHEIYSP 60
 QY 61 TTTTSMYDDYQKTGIDLWRTHEESKMDTLKLEINNKLRREIRQRLGHDNLGSLSPDE 120
 Db 61 NTTTKMIDLYRITGLVDIMNKGHEKQENLRDLINNKLRREIRQRTGDEMSGLNQE 120
 QY 121 LASLDDMOSSLDARQKTHVYKTQETETTKKVKYKLEQRGNMLHGFDOEAGEDEPQY 180
 Db 121 LCHLQGNVSDSLAEIRERKTHVYKTQETCRKRVNLEORGNMLHGFDOEAGEDEPQY 177
 QY 181 GYEDNEGDYESALALNSGANNLYTFHLH--HPNLHHGSSLSGSIITLHDLRLA 232
 Db 178 GYVNEGDYESVALANGASNLTFPNRVHNNHLDHGGGSLVSYTLHONPNHGNH 236

RESULT 5

Q9ZS28 PRELIMINARY; PRT; 226 AA.
 AC Q9ZS28: PRELIMINARY; PRT; 226 AA.
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE MADS-box protein, GDEF1.
 OS Gerbera hybrida.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Campanulids; Asterales; Asteraceae; Multisididae; Gerbera.
 CC NCBI_TaxID=18101;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=CV. Terra Regina;
 RA MEDLINE=9168221; Pubmed=10069067;
 RA Yu D., Kotilainen M., Poellänen E., Mehto M., Elomaa P.,
 RA Helariutta Y., Albert V.A., Teeri T.H.;
 RT "Organ identity genes and modified patterns of flower development in Gerbera hybrida (Asteraceae)."
 RT Plant J. 17:51-62(1999).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
 DR EMBL; AJ009724; CAA08802.1; -.
 DR HSP; P11746; IMNM.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRP-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS00066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 KM SEQUENCE 226 AA; 26556 MW; 1C2553CB85E4B997 CRC64;

Query Match 59.3%; Score 721.5; DB 10; Length 226;
 Best Local Similarity 63.0%; Pred. No. 1.9e-48;
 Matches 145; Conservative 24; Mismatches 50; Indels 11; Gaps 4;

QY 1 MARGKIEIKLIENTRQVYTSKRNGIFPKAQELTVLCAKYSILMLSTNNMHEIYSP 60
 Db 1 MARGKIEIKLIENTRQVYTSKRNGIFPKAKELTVLCAKYSILMLSTNNMHEIYSP 60
 QY 61 TTTTSMYDDYQKTGIDLWRTHEESKMDTLKLEINNKLRREIRQRLGHDNLGSLSPDE 119
 Db 61 STTTTKMYDDYQKTGIDLWRTHEESKMDTLKLEINNKLRREIRQRLGHDNLGSLSPDE 120
 QY 120 ELASLDDMOSSLDARQKTHVYKTQETETTKKVKYKLEQRGNMLHGFDOEAGEDEPQY 178
 Db 121 DLTSLEGMODSLTLVRERKTHVYKTQETCRKRVNLEORGNMLHGFDOEAGEDEPQY 177
 QY 179 QYEDNEGDYESALALNSGANNLYTFHLHHPNLHHGSSLSGSIITLHDLRLA 228
 Db 178 KYDTGENEGDYESVALANGASNLTFPNRVHNNHLDHGGGSLVSYTLHONPNHGNH 236

RESULT 6

Q65211 PRELIMINARY; PRT; 227 AA.
 AC Q65211: PRELIMINARY; PRT; 227 AA.
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE PTD protein.

OS Populus trichocarpa (Western balsam poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
 OX NCBI_TaxID=3694;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20484033; PubMed=11027713;
 RA Sheppard L.A., Brunner A.M., Krutovskii K.V., Rottmann W.H.,
 RA Skinner J.S., Voliner S.S., Strauss S.H.,
 RT "A DIVERGENT Homolog from the Dioecious Tree Black Cottonwood is
 RT Expressed in Female and Male Floral Meristems of the Two-Whorled,
 RT Unisexual Flowers."
 RL Plant Physiol. 124:627-640(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sheppard L.A.;
 RT "PTD: A Populus trichocarpa gene with homology to floral homeotic
 RT transcription factors."
 RL Thesis (1997), Oregon State University, Corvallis, OR, USA.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL; AF057708; AAC13695.2; -.
 DR HSSP; P11746; 1MM.
 DR TRANSFAC; T04746; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR Pfam; PF00319; SRP-TF; 1.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS00065; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 227 AA; 26394 MW; 6E62247A629753CA CRC64;
 Query Match 58.3%; Score 709.5; DB 10; Length 227;
 Best Local Similarity 62.3%; Pred. No. 1.6e-47;
 Matches 149; Conservative 24; Mismatches 45; Indels 21; Gaps 5;
 QY 1 MARGEKIKLENTQNTQVYTSKRNGIFPKAQLTYLCPAKYSLIMLSTNKHETISPTT 60
 DB 1 MGRGKIKLENTQNTQVYTSKRNGIFPKAQLTYLCPAKYSLIMLSTNKHETISPTT 60
 QY 61 TTTKSYDYQKTMGIDLWRTHEESKQTLWKKEINNTLRREIRORLGHDLNGSLFPE 120
 DB 61 STSTFKYDYQKTMGIDLWRTHEESKQTLWKKEINNTLRREIRORLGHDLNGSLFPE 120
 QY 121 LASTIDEMQSLDAIRQKXHVITQETETTKKVKVNLQORGNMLHGYFPOEAAAGEDPOY 180
 DB 121 LRGLQCHMTBALNGVRKXHVITQETETTKKVKVNLQORGNMLHGYFPOEAAAGEDPOY 180
 QY 121 LRGLQCHMTBALNGVRKXHVITQETETTKKVKVNLQORGNMLHGYFPOEAAAGEDPOY 177
 DB 121 LRGLQCHMTBALNGVRKXHVITQETETTKKVKVNLQORGNMLHGYFPOEAAAGEDPOY 177
 QY 181 GYEDNEGYSALALSGANNLYTFHLH-----PMLHGGSSLGSSITHLDLRL 231
 DB 178 GLVDN-----EAAVALANGASNLVAFRLHGHNNHHHLPMLH-LGDGFGA-----HELRL 226
 RESULT 7
 ID Q040171 PRELIMINARY; PRT; 222 AA.
 AC Q040171;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE TDR6 protein (Fragment).
 GN TDR6.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93251098; PubMed=1688249;
 RA Pnueli L., Abu-Abeid M., Zamir D., Nacken W., Schwarz-Sommer ZS.,
 RA Lifschitz E.;
 RT "The MADS box gene family in tomato: temporal expression during floral
 RT development, conserved secondary structures and homology with homeotic
 RT genes from Antirrhinum and Arabidopsis."
 RL Plant J. 1:255-266(1991).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL; X60759; CAA43171.1; -.
 DR PIR; S23731; S23731.
 DR HSSP; P11746; 1MM.
 DR TRANSFAC; T03188; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRP-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS00065; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 FT NON TER 1
 SQ SEQUENCE 222 AA; 25820 MW; CD22DD7E23DD1E0D CRC64;
 Query Match 56.8%; Score 690.5; DB 10; Length 222;
 Best Local Similarity 59.7%; Pred. No. 4.8e-46;
 Matches 138; Conservative 29; Mismatches 53; Indels 11; Gaps 4;
 QY 4 GKIEIKLENTQNTQVYTSKRNGIFPKAQLTYLCPAKYSLIMLSTNKHETISPTT 63
 DB 1 GKIEIKLENTQNTQVYTSKRNGIFPKAQLTYLCPAKYSLIMLSTNKHETISPTT 60
 QY 64 TKSMTDYQKTMGIDLWRTHEESKQTLWKKEINNTLRREIRORLGHDLNGSLFPELAS 123
 DB 61 TKKMTDYQKTMGIDLWRTHEESKQTLWKKEINNTLRREIRORLGHDLNGSLFPELAS 120
 QY 124 LDDENQSLDAIRQKXHVITQETETTKKVKVNLQORGNMLHGYFPOEAAAGEDPOY 183
 DB 124 LQENITSEVAIRERKXHVITQETETTKKVKVNLQORGNMLHGYFPOEAAAGEDPOY 177
 QY 184 DNEGDEBESALALSGANNLYTFHLH--HPMLHGGSSLGSSITHLDLRLA 232
 DB 178 ENEGHYSAAVAFANGVNLVAFRLQPLHPLQNEG-GFGS-----RDLRLS 222
 RESULT 8
 ID Q8H282 PRELIMINARY; PRT; 222 AA.
 AC Q8H282;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE TDR6 transcription factor (Fragment).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Platense; TISSUE=fruit;
 RA Busi M.V., D'Angelo M.C., Hidalgo-Cuevas M., Bustamante C.A.,

RA Boggio S., Valle E., Zabaleta E.J.;
 RT "MADS-box genes expressed during the tomato seed and fruit
 development."
 RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY038734; AAM3100.2; -
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADS_DOMAIN.
 DR SMART; SM00432; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 FT NON_TER
 SQ SEQUENCE 222 AA; 25843 MW; 67E61AA125812A08 CRC64;

Query Match 56.8%; Score 690.5; DB 10; Length 222;
 Best Local Similarity 59.7%; Pred. No. 4,8e-46;
 Matches 138; Conservative 30; Mismatches 52; Indels 11; Gaps 4;

QY 4 GKEIKLLENQTRQVYSKRRNGIFKKAQELTVLCAKVSILMLSTNKKHEIYISPTT 63
 DB 1 GKEIKLLENQTRQVYSKRRNGIFKKAQELTVLCAKVSILMLSTNKKHEIYISPTT 60
 QY 64 TKSVDYDQKTMGIDLMRTHEESMKTLMKKEINNKLRREIRQLGHDNGLSFDEIAS 123
 DB 61 TRKMDYQASALGVDIWIIHERKQENLRKLEINNKLRREIRQLGHDNGLSFDEIAS 120
 QY 124 LDDEMOSSLDIAIRCKRYHVIKTQETETKKKYNLEQRGNMLHGYFDEAAGDPQYGE 183
 DB 121 LGENTSEVAIEIREKHVINKQDTCCKKARNLEQNGNLV---LDLEACEDPKYGVV 177
 QY 184 DNEGDYESALALSGANNLYTFHLH--HPNLIHGSSISGSSITTHLDIRLA 232
 DB 178 ENEGHYSAVAFANGVHNLVAFRLQPLHPNLQNEG--GFGS-----RDLRLS 222

RESULT 9

Q84U28 PRELIMINARY; PRT; 238 AA.

AC Q84U28; 01-JUN-2003 (TREMBLrel. 24, Created)

DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC Eucosids I; Malpighiales; Salicaceae; Salicaceae; Populus.

NCBI_TaxID=118781;

SEQUENCE FROM N.A.

RA An X., Zhang Z., Li S.;

RT "Molecular cloning of APTALA3 (AP3) homologous gene from male poplar

(Populus tomentosa Car.)."

RL Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.

DR EMBL; AY210488; AAO49713.1; -

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR002487; TF_Kbox.

DR InterPro; IPR002100; TF_MADSbox.

DR Pfam; PF01486; K-box; 1.

DR Pfam; PF00319; SRF-TF; 1.

DR PRINTS; PR00404; MADS_DOMAIN.

DR SMART; SM00432; MADS_BOX_1; 1.

DR PROSITE; PS50066; MADS_BOX_2; 1.

DR PROSITE; PS50066; MADS_BOX_2; 1.

SEQUENCE 238 AA; 27207 MW; 20EBA028350A4FE7 CRC64;

Query Match 56.1%; Score 682; DB 10; Length 238;

Best Local Similarity 58.5%; Pred. No. 2.4e-45;
 Matches 144; Conservative 28; Mismatches 50; Indels 24; Gaps 4;

QY 1 MARGKIEIKLENTQTRQVYSKRRNGIFKKAQELTVLCAKVSILMLSTNKKHEIYISPTT 60
 DB 1 MARGKIEIKLENTQTRQVYSKRRNGIFKKAQELTVLCAKVSILMLSTNKKHEIYISPTT 60
 QY 61 TTTTSSVYDQKTMGIDLMRTHEESMKTLMKKEINNKLRREIRQLGHDNGLSFDEIAS 120
 DB 61 TTTTSSVYDQKTMGIDLMRTHEESMKTLMKKEINNKLRREIRQLGHDNGLSFDEIAS 120
 QY 121 LRLGDMHTBALGVGRKHVITKTQETETKKKYNLEQRGNMLHGYFDEAAGDPQY 180
 DB 121 LRLGDMHTBALGVGRKHVITKTQETETKKKYNLEQRGNMLHGYFDEAAGDPQY 177
 QY 181 GYEDNE-----GDYESALALSGANNLYTFHLHHPNLIHGSSISGSSITTHL----- 226
 DB 178 GLVDNEAAVALVDGASDNEAAVALADGASNLVAILRHGHNNHHPN-----LHLEDGFG 231
 QY 227 -HDLRL 231
 DB 232 AHELR 237

RESULT 10

Q9LLA2 PRELIMINARY; PRT; 201 AA.

AC Q9LLA2; 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DE MADS box transcription factor TW6 (Fragment).

OS Hydrangea macrophylla.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Cornales; Hydrangeaceae; Hydrangea.

NCBI_TaxID=23110;

SEQUENCE FROM N.A.

RA Kramer E.M., Irish V.F.;

RT "Evolution of the petal and stamen developmental programs: Evidence

from comparative studies of the lower eudicots and basal

angiosperms."

RL Int. J. Plant Sci. 0:0-0(2000).

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION

FACTORS.

DR EMBL; AF230703; AAF73932.1; -

DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR002487; TF_Kbox.

DR InterPro; IPR002100; TF_MADSbox.

DR Pfam; PF01486; K-box; 1.

DR Pfam; PF00319; SRF-TF; 1.

DR SMART; SM00432; MADS_BOX_1; 1.

DR PROSITE; PS50066; MADS_BOX_2; 1.

DR PROSITE; PS50066; MADS_BOX_2; 1.

SEQUENCE 201 AA; 23226 MW; 66928A89200A042 CRC64;

Query Match 54.2%; Score 659; DB 10; Length 201;
 Best Local Similarity 62.2%; Pred. No. 1.2e-43;
 Matches 130; Conservative 25; Mismatches 44; Indels 10; Gaps 3;

QY 26 NGIFKKAQELTVLCAKVSILMLSTNKKHEIYISPTTTSKVDYDQKTMGIDLMRTHEE 85
 DB 1 NGIFKKAQELTVLCAKVSILMLSTNKKHEIYISPTTTSKVDYDQKTMGIDLMRTHEE 80
 QY 86 SMKDTLMKLEINNKLRREIRQLGHDNGLSFDEIASLDDEMOSSLDIAIRCKRYHVIKT 145
 DB 61 RMQEHRLKLEKVNKLRRREIRQLGHDNGLSFDEIASLDDEMOSSLDIAIRCKRYHVIKT 120

Qy 146 QTEETKKKKKRLLEORGNMLHGYPDEAGDPQYGEYEDNEGYESALALNSGANNLYTF 205
 Db 121 QTEETCKKKKRLLEORGNMLHGYPDEAGDPQYGEYEDNEGYESALALNSGANNLYTF 177
 Qy 206 HLH--HPLNHHGGSSLLGSSITLHDLRLA 232
 Db 178 GLQPSHPLHGGGGGGS-----HDLRLA 201

RESULT 11

ID Q40513 PRELIMINARY; PRT; 227 AA.
 AC Q40513;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE MADS-box protein.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Nicotiana.
 CC NCBI_Taxid=4097;
 RN [1]
 RE SEQUENCE FROM N.A.
 RA MEDLINE=97046712; PubMed=8893543;
 RT "Alteration of tobacco floral organ identity by expression of
 combinations of Antirrhinum MADS-box genes."
 RL Plant J. 10:653-677(1996).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 DR EMBL: X96428; CAA65288.1; -.
 DR HSSP; P11746; IMM.
 DR TRANSFAC; T03109; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00404; MADSOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS0066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 227 AA; 26401 MW; FEF88A9A2AD7FEC4 CRC64;

Query Match 52.5%; Score 638; DB 10; Length 227;
 Best Local Similarity 56.3%; Pred. No. 6.1e-42;
 Matches 129; Conservative 36; Mismatches 52; Indels 12; Gaps 5;

Qy 1 MARGKIEIKLIENQTNQVYTSKRNGIFKKAQELTVLCPDAKSLIMLSTNKGHEYISP 60
 Db 1 MARGKIQIKLIENQTNQVYTSKRNGIFKKAQELTVLCPDAKSLIMLSTNKGHEYISP 60
 Qy 61 TTTTKSMYDYOXTMGIDLMRTHEESKMDTLMLKEINNKLRRIROGLHDNLGSLFDE 120
 Db 61 SVTTKQFLDYQKTVGIDLMNSHKKQEQRLKLDVNRNLRRIROGLHESLNDLNFQ 120
 Qy 121 LASIDDEMOSSLDAIRORXKRVHVIKTQETTKKKVKNLEORGNMLHGYPDEAGDPQY 180
 Db 121 LEELNENVDNSLKLIRERKRVKVIQNGQIDTYKKVAVNEIEHRLN---LEFDARQEDPYG 176
 Qy 181 GYEDNEGYESALALNSGANNLYTFHL---HPLN--LHHGSSLLGSSIT 224
 Db 177 GLVQEGDYNVSLGFPNGSPRIILRLQPMHQPNNHHHLSG---GSDIT 222

RESULT 12

Q41417
 ID Q41417 PRELIMINARY; PRT; 228 AA.
 AC Q41417;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Deficiens analogue.
 GN DEF4.
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 CC NCBI_Taxid=4113;
 RN [1]
 RE SEQUENCE FROM N.A.
 RA STRAIN=Granola; TISSUE=leaf;
 RC MEDLINE=94100991; PubMed=7903890;
 RT Garcia-Maroto F.; Salami F.; Robde W.;
 RT "Molecular cloning and expression patterns of three alleles of the
 Deficiens-homologous gene St-deficiens from Solanum tuberosum."
 RL Plant J. 4:771-780(1993).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.

DR EMBL: X67511; CAA47846.1; -.
 DR PIR; T07066; T07066.
 DR HSSP; P11746; IMM.
 DR TRANSFAC; T03179; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR PRINTS; PR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00404; MADSOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS0066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 228 AA; 26367 MW; 8568024C423BE93F CRC64;

Query Match 51.7%; Score 628.5; DB 10; Length 228;
 Best Local Similarity 54.1%; Pred. No. 3.4e-41;
 Matches 124; Conservative 40; Mismatches 54; Indels 11; Gaps 3;

Qy 1 MARGKIEIKLIENQTNQVYTSKRNGIFKKAQELTVLCPDAKSLIMLSTNKGHEYISP 60
 Db 1 MARGKIQIKLIENQTNQVYTSKRNGIFKKAQELTVLCPDAKSLIMLSTNKGHEYISP 60
 Qy 61 TTTTKSMYDYOXTMGIDLMRTHEESKMDTLMLKEINNKLRRIROGLHDNLGSLFDE 120
 Db 61 SITTKQFLDYQKTVGIDLMNSHKKQEQRLKLDVNRNLRRIROGLHESLNDLNFQ 120
 Qy 121 LASIDDEMOSSLDAIRORXKRVHVIKTQETTKKKVKNLEORGNMLHGYPDEAGDPQY 180
 Db 121 LEELNENVDNSLKLIRERKRVKVIQNGQIDTYKKVAVNEIEHRLN---LEFDARQEDPYG 177
 Qy 181 GYEDNEGYESALALNSGANNLYTFHL---HPLNHHGGSSLLGSSIT 224
 Db 178 GLVQEGDYNVSLGFPNGSPRIILRLQPMHQPNNHHHLSG---GSDIT 223

RESULT 13

ID Q41477 PRELIMINARY; PRT; 228 AA.
 AC Q41477;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Deficiens analogue.

Query Match	51.4%	Score 624.5	DB 10	Length 228
Best Local Similarity	53.7%	Pred. 6.9e-41		
Matches 123	Conservative 41	Mismatches 54	Indels 11	Gaps 3
QY	1	MARGKIEIKLEIKENQTRQVYYSKRNGSFFKKAQELTVCDPKAVLMLSTNVCHEIYSP	60	
DB	1	MARGKQIKIKIENQTRQVYYSKRNGSFFKKAQELTVCDPKAVSIVWISSTGTLHEFISP	60	
QY	61	TTTTKSMYDDYQXTWAGIDLMRTHESSMDLIWKLKEINNKLRREIRQRLGHDNGSLFDE	120	
DB	61	SITTNLFLFDYQGTICVDITWISHYEMQEQLRKLDVYNNLRKEIRQRMGESINDINFPQ	120	
QY	121	LAALDEMOSSLDPAIRQKRYHYIKQYETTKKKYKYNLEQRGNMLHGYFPOEAAAGDPQY	180	
DB	121	LEELMENVNSLTLIRERKXKVIQNIETRYKQVNNVEIHRNLL--LEFDARQDPYQ	177	
QY	181	GYEDNEGDEYSALATNSGNNLYTFHL-----HHNHLHGSSLSGSSIT	224	
DB	178	GLVEQEGDYNSTVLGPTGGHILLALGLQDPNNHHHLLHSGS--GSDIT	223	

RESULT 14

ID	Q40352	PRELIMINARY	PRT	247 AA.
AC	Q40352			
DT	01-NOV-1996	(TEMBREL. 01, Created)		
DT	01-MAY-1997	(TEMBREL. 03, Last sequence update)		
DT	01-JUN-2003	(TEMBREL. 24, Last annotation update)		
DE	MADS-box protein.			
OS	Medicago sativa (alfalfa).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid 1; Fabiales; Fabaceae; Papilionoideae; Trifoliales; Medicago.			
OX	NCBI_TaxID=3879.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Node;			
EX	MEDLINE=95296292; PubMed=7777496;			
HA	Heard J., Dunn K.;			

	Query Match	51.3%	Score 623.5;	DB 10;	Length 247;
	Best Local Similarity	54.4%;	Pred. No. 9.2e-41;		
	Matches 123;	Conservative 35;	Mismatches 63;	Indels 5;	Gaps 2;
Qy	1 MARGKIEIKLEIENOTNRQVTVYSKRPNGIFFKAQOELATLCPDAKSYSLIMASTNKHEEYISP	60			
Dd	1 MARGKIQRKIENITNRRQVIYSKRPNGLFFKANHELVLCPAKSYLIINFSSIGKLHEEYISP	60			
Qy	61 TTTTTSKYDDYDQKTMGIDILMRTHEESMKDTLMUKLEINNTKLRREIRRLRGLHDNLGSLFDE	120			
	: : : :				
	: : : : :				
Dd	61 SASSTKFDPDYQTTVGIDLSNHSYEKNQENLKLDKVNNRLRREIRFGMGECNDLSEEE	120			
	: : : :				
	: : : : :				
Qy	121 IASLDDEMGSLLAIROKRYHVIKTQETETTKKKVKONLEPGRGNMLHGYPFOEAAAGSDPOY	180			
	: : : :				
	: : : : :				
Dd	121 LRLEDDEMDKALVAIERKKYKVTITNQDTRKKFFNNEREVDNRLLR---DLDAEAEDPRF	177			
	: : : :				
	: : : : :				
Qy	181 GYEDNEGDYSESALALSNGANNLYTFHLH--HPNLIHQSGSSLGSSIT	224			
	: : : :				
	: : : : :				
Dd	178 EMMDNNGGEYESVGFSNLGPRMALSIQTPHHPPHNNGAASAADULT	223			
	: : : :				
	: : : : :				

```

RESULT 15
ID O65141 PRELIMINARY; PRT; 228 AA.
AC O65141;
DT 01-AUG-1998 (TrEMBLrel_07, Created)
DT 01-AUG-1998 (TrEMBLrel_07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel_24, Last annotation update)
DE APETAL3 homolog PAAP3-2.
OS Papaver nudicaule.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
OC Papaveraceae; Papaver.
CX NCBI_TaxID=74823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278797; PubMed=9611190;
RA Kramer E.M., Dorit R.L., Irish V.F.;
RT "Molecular evolution of genes controlling petal and stamen
RT development: duplication and divergence within the APETAL3 and
RT PISTILLATA MADS-box gene lineages.";
RL Genetics 149:765-783(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
DR EMBL; AF052874; AAC42589.1; -.

```

DR HSSP; P11746; 1MM.
 DR TRANSFAC; T03139; -
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01466; K-box; 1.
 DR Pfam; PF00319; SRF-1F; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS0066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription; Transcription regulation.
 SQ SEQUENCE 228 AA; 26501 MM; 22405D9783465CE5 CRC64;

Query Match 51.2%; Score 623; DB 10; Length 228;
 Best local similarity 54.2%; Pred. No. 9,1e-41;
 Matches 128; Conservative 38; Mismatches 58; Indels 12; Gaps 4;

QY 1 MARGKIKLIENOTNRQVYSKRRNGIFPKAQLTVLCDAKVSLIMSTNKGHEVISP 60
 DB 1 MGRKIKIKLIENATNRQVYISKRSGILKKAKELIVLCDAEVSLIFSGTGYELSP 60
 QY 61 TT--TYSMYDDYQKTMGIDLMRTHESSMDTLMLKLEINNKLRREIRQRLGHDLNLSF 118
 DB 61 SLNGNTKRYVDKYQQLSGISIMNSHYESLQNALNKQKEINRRLREIRQRMGEDLDELTI 120
 QY 119 DELASLDDEMSSLDALRQKRYHVIKTQETTTKKRYNLEQRRGNMLHGTFDEALAGDP 178
 DB 121 EELRSLQNLLEASVYKVRDRKHVILITQETTRKLNHTEQNHGLREF--EPILDEDP 178
 QY 179 QYGEDNEGDYESALALNSGANNLYTFHLH--HPNLHGSSSLGSSITHLHDLRLA 232
 DB 179 HYVIAHQEDYESALIELAHGPNIFAFRLQPSQPNLHNGG-----YNCHDLRLA 228

Search completed: September 27, 2004, 09:28:17
 Job time : 76.7383 secs

GenCore version 5.1.6
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OW protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2004, 04:52:23 ; Search time 3964.76 Seconds
(without alignments)
2536.240 Million cell updates/sec

Title: US-10-069-527-4
Perfect score: 1216
Sequence: 1 MARKIEIKLENTNRQVT.....HHGSSIGSSITLHDLRLA 232

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2.1/USPTO.spoos/US10069527/runat.23092004.163623.5742/app.query.fasta_1.782
-DB=GenEmbl -OPWT=fastap -SUFFIX=rgs -WINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR.SCORE=PCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=PCT -NOM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10069527@cgn2.1.1.3998 @runat.23092004.163623.5742 -NCPU=6 -ICPU=3
-NO.WMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl :
1: gb_ba :
2: gb_hcg :
3: gb_in :
4: gb_cm :
5: gb_ov :
6: gb_pal :
7: gb_ph :
8: gb_pl :
9: gb_pr :
10: gb_ro :
11: gb_scs :
12: gb_sy :
13: gb_un :
14: gb_vl :
15: gb_ba :
16: em_fun :
17: em_hum :
18: em_mu :
19: em_mu :
20: em_mu :
21: em_or :
22: em_ov :
23: em_pat :
24: em_ph :
25: em_pl :
26: em_ro :
27: em_scs :
28: em_un :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1203	98.9	1102	8	MDC251116
2	1072.5	88.2	1043	8	AB081093
3	882.5	72.6	1014	8	AB055966
4	721.5	59.3	906	8	GHY9724
5	721.5	59.3	994	8	AF230704
6	709.5	58.3	681	6	AR372459
7	709.5	58.3	946	6	AR372458
8	690.5	56.8	895	6	LEIDR6
9	690.5	56.8	945	8	AY098734
10	667.5	54.9	998	8	AMDEFI
11	659	54.2	939	8	AF230703
12	641.5	52.8	881	8	PHGP
13	638	52.5	1113	8	NTMADSBX
14	624.5	51.4	924	8	STPD4
15	623.5	51.3	965	8	ALFMBP
16	623	51.2	1008	8	AF052874
17	616.5	50.7	1005	6	AX478039
18	616	50.7	1006	8	AB071378
19	612	50.3	1039	8	AF503913
20	612	50.3	1129	8	AB099875
21	608.5	50.0	830	8	AY397762
22	600.5	49.4	833	8	AF209729
23	597	49.1	1002	8	AB094965
24	595	48.9	852	8	AB050649
25	590.5	48.6	952	8	AB094964
26	577	47.5	1016	8	AB094966
27	575	47.3	875	8	AF180364
28	575	47.3	839	8	AB090863
29	572.5	47.1	939	8	BOU67453
30	569.5	46.8	812	8	AF052869
31	569	46.8	793	8	AB090867
32	569	46.8	811	8	AB090865
33	569	46.8	844	8	AY173070
34	569	46.8	959	8	AY087369
35	566	46.5	687	8	AF180365
36	566	46.5	785	8	AF052875
37	564	46.4	730	8	AY142590
38	564	46.4	960	8	AY070397
39	564	46.4	1010	8	ATHAPETELA
40	563	46.3	921	8	GHY9725
41	562.5	46.3	921	8	AY173060
42	562	46.2	976	8	SLSLM3
43	561.5	46.1	696	8	AY173064
44	561	46.1	753	8	AY162861
45	560.5	46.1	941	8	AF124814

ALIGNMENTS

RESULT 1

MD0251116 1102 bp mRNA linear PLN 16-NOV-2001
 LOCUS MD0251116
 DEFINITION Malus domestica mRNA for B-type MADS box protein (mads13 gene).
 ACCESSION AJ251116
 VERSION AJ251116.1 GI:16973293
 KEYWORDS B-type MADS box protein; mads13 gene.
 SOURCE Malus x domestica (apple tree)
 ORGANISM Malus x domestica
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; euroside I; Rosales; Rosaceae; Maloideae; Malus.
 REFERENCE 1
 AUTHORS Vosman, B. and Smulders, M.J.M.
 TITLE Isolation of apple B- and C-type MADS box genes from vegetative
 tissue
 JOURNAL unpublished
 REFERENCE 2 (bases 1 to 1102)
 AUTHORS van der Linden, C.G.
 TITLE Direct Submission
 JOURNAL Submitted (15-NOV-1999) van der Linden C.G., Identity and Genetic
 Diversity, CPRO Wageningen University & Research Centre, PO Box 16,
 Wageningen, 6700 AR, NETHERLANDS
 FEATURES
 source Location/Qualifiers
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 71..769
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 ORIGIN
 Alignment Scores:
 Pred. No.: 4,78e-101 Length: 1102
 Score: 1203.00 Matches: 230
 Percent Similarity: 99.14% Conservative: 0
 Best Local Similarity: 99.14% Mismatches: 2
 Query Match: 98.93% Indels: 0
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 US-10-069-527-4 (1-232) x MD0251116 (1-1102)
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 QY 21 TysSerIysArgIsgAngIyIlePheIySlyAlaGlnGluLeuThrValIeuCysAsp 40
 Db 131 TACTCCAAAGAGAAATGAGATCTTCAGAAAGAGCTCAGAGGTCAACGTTCTCTGTAT 190
 QY 41 AlAlaYValSerIleuIleMetLeuSerAsnThrAsnLysMetHisGluTrIleSerPro 60
 Db 191 GCCAAGGTCTCCCTCATATGCTCTCCCAACAAATTAATGACACAGATATACAGCCCT 250
 QY 61 ThrThrThrThrIysSerMetIYrAspAspIYrGlnIySThrMetGlyIleAspLeuTrp 80
 Db 251 ACCACTTCGACCAAGAGTATGATGACTATCAGAAAACHTATGGGATTCATCTGTGG 310
 QY 81 ArgThrHisGluIuSerMetLysAspThrLeuTrpLysLeuIleGluIleAsnLys 100

Db 311 AGGACACAGAGAGATCATGAAAGACCTTGTGGAGTTGAAAGATCAACAATATAG 370
 QY 101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
 Db 371 CTGAGAGAGAGATCAGACGAGGTTGGCCATGATCTTAATGAGCTTGAGCTTGACGAG 430
 QY 121 LeuAlaSerLeuAspAsnGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTrp 140
 Db 431 CTGGCTTCTCTTGACGATGATGATGAGCTTCTCTGATGTCATACGTCAAAGAAAGTAC 490
 QY 141 HisValIleIySthrgInThrGluThrThryIySlySlyValIyAsnLeuGluArg 160
 Db 491 CATGATCAAAACCTCAACAGGAGACCAAGAAAGGTTAAGACTTGAGACCAAGA 550
 QY 161 ArgGlyAsnMetLeuHisGlyTrpPheAspGlnGluAlaAlaGlyGluAspProGlnTrp 180
 Db 551 AGAGAAACATGCTGCAGACGCTATTTTGCACGAGAGAGCGGCGAGACCCACAGTAT 610
 QY 181 GlyTrpGluAspAsnGluIyAspTyGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
 Db 611 GGTATGAGACATGAGGAGGACTACGAACTTCGACTTGATTCATTAATGGGCGCAT 670
 QY 201 AsnLeuTrpThrPheHisLeuHisIleProAsnLeuHisHisGlyIySerSerLeuGly 220
 Db 671 AACTGTACACTTTCACCTCCACACCGCTAACCTCCACACGAGAGAAAGTTCCGCTCGC 730
 QY 221 SerSerIleThrHisIleuHisAspLeuArgLeuAla 232
 Db 731 TCTTCATTTACTCATCTGCACGATCTCGGCTTCTCT 766
 RESULT 2
 AB081093 1043 bp mRNA linear PLN 06-SEP-2002
 LOCUS AB081093
 DEFINITION Malus x domestica MdTM6 mRNA for MADS-box protein, complete cds.
 ACCESSION AB081093
 VERSION AB081093.1 GI:22775407
 KEYWORDS
 ORGANISM
 SOURCE
 Malus x domestica (apple tree)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; euroside I; Rosales; Rosaceae; Maloideae; Malus.
 REFERENCE 1
 AUTHORS Matsumoto, S., Ohtsubo, T. and Soejima, J.
 TITLE Cloning and sequencing of apple MADS-box genes 'Md12P', 'MdTM6' and
 'MdMADS13'
 JOURNAL unpublished
 REFERENCE 2 (bases 1 to 1043)
 AUTHORS Ohtsubo, T. and Matsumoto, S.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAR-2002) Shogo Matsumoto, Gifu University,
 Department of Biology, Faculty of Education; 1-1, Yanagido, Gifu,
 Gifu 501-1193, Japan (E-mail:shmatsumo@gcc.gifu-u.ac.jp,
 Tel:81-58-293-2257, Fax:81-58-293-2207)
 FEATURES
 source Location/Qualifiers
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 63..776
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RGNNLHGVEASENPOYCYVDNEGDYESALVLANGANNLYTFOJHRNSDQLHHPNLHH
HRSGLSSSTHLDRLA"

ORIGIN

Alignment Scores: 4.02e-89 Length: 1043
Pred. No.: 1072.50 Matches: 211
Score: 91.67% Conservative: 9
Percent Similarity: 87.92% Mismatches: 9
Best Local Similarity: 88.20% Indels: 11
Query Match: 8 Gaps: 3

US-10-069-527-4 (1-232) x AB081093 (1-1043)

QY 1 MetAlaArgGlyLysIleGluIleuLeuIleGluAsnGlnThrAspArgGlnValThr 20
DB 63 ATGGGTCTGGAAGATTGAGATCAAGCTGATCAAAAACGACCAACAGGCAAGTACC 122
QY 21 TySerLysArgAsnGlyIlePheLysAlaGlnGlnLeuThrValLeuCyasp 40
DB 123 TACTCCAGAGAGAAATGGATCTTCAGAAAGCTCAGAGCTCACCGTTCTGTGAT 182
QY 41 AlAlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
DB 183 GCCAAGGCTCCCTCATCATGCTCTCCAACTAGTAAATGACAGATATATCAGCCCT 242
QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyLeuAspLeuTyr 80
DB 243 ACCACTACGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 302
QY 81 ArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnAsnLys 100
DB 303 AGGACACACTACGATCATGATGATGATGATGATGATGATGATGATGATGATGATG 362
QY 101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
DB 363 CTGGAGAGAGATCAGGAGAGATGAGGAGATGAGGAGATGAGGAGATGAGGAGATG 422
QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
DB 423 CTCGGTCTCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 482
QY 141 HisValIleLysThrGlnThrGlnThrThrLysLysLysValLysAsnLeuGlnArg 160
DB 483 CATGATGATCAAACTCAAAACGAGACCAAGAAAGAGGTTAAGAACTTGAGAGAAAGA 542
QY 161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGlnAlaIleArgLysAspProGlnTyr 180
DB 543 AGAGGAACATGCTCCATGCTAT-----GAGCTGCCAGTGAAGAACCCACATAT 593
QY 181 GlyTyrGluAspAsnGlnGlyAspTyrGlnSerAlaLeuAlaLeuSerAsnGlyValAsn 200
DB 594 TGTATGTGGCAATGAGGAGAGACTATGATCTGCTGCTGCTGCTGCTGCTGCTGCT 653
QY 201 AsnLeuTyrThrPhe-----HisLeuHisAspProAsnLeu--- 212
DB 654 AACTGTACACTTTCAGACTCCACCGCACTCCGACAGCTCCACACCTTAACCTTCAC 713
QY 213 HisHisGlyLysSerSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLeuAla 232
DB 714 CACCAAGAGAGAGATGCTCGCTCGCTCCCTCCATCATCATCATCATCATCATCATCAT 773
RESULT 3
AB055966 1014 bp mRNA linear PLN 07-NOV-2001
LOCUS ROSA rugosa MASAKO B3 mRNA for MADS-box protein, complete cds.
DEFINITION
AB055966
ACCESSION
AB055966.1 GI:15216292
VERSION
KEYWORDS
SOURCE
ORGANISM
Rosa rugosa
Rosa rugosa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE

1 Kitahara, K., Hirai, S., Fukui, H. and Matsumoto, S.
Rose MADS-box genes 'MASAKO Bp and B3' homologous to class B floral
identity genes
Plant Sci. 161, 549-557 (2001)
2 (bases 1 to 1014)
Matsumoto, S., Hirai, S. and Kitahara, K.
Submitted (19-FEB-2001) Shogo Matsumoto, Gifu University,
Department of Biology, Faculty of Education, 1-1, Yanagido, Gifu,
Gifu 501-1193, Japan (E-mail: shmatsumo@cc.gifu-u.ac.jp,
Tel:81-58-293-2257, Fax:81-58-293-2207)

JOURNAL

TITLE

AUTHORS

JOURNAL

FEATURES

source

1. 1014
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ORIGIN

Alignment Scores: 9.85e-72 Length: 1014
Pred. No.: 882.50 Matches: 174
Score: 75.29% Conservative: 24
Percent Similarity: 72.16% Mismatches: 32
Best Local Similarity: 72.57% Indels: 33
Query Match: 8 Gaps: 3

US-10-069-527-4 (1-232) x AB055966 (1-1014)

QY 1 MetAlaArgGlyLysIleGluIleuLeuIleGluAsnGlnThrAspArgGlnValThr 20
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DB 105 TATTCAGAGAGAGAAATGGATCTTCAGAAAGCTCAGAGCTCACGGTCTGTGTGAC 164
QY 41 AlAlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
DB 165 GCTCAGTCTCCTCATCATGATGATGATGATGATGATGATGATGATGATGATGATG 224
QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyLeuAspLeuTyr 80
DB 225 ACCACTACGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 284
QY 81 ArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnAsnLys 100
DB 285 AGCTCACTACAGGCAATGAAAGAACTTGTGAAACTGAAAGAGTTAAACATTAAG 344
QY 101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
DB 345 CTGAGAGAGGACATCAGGCAAGGCTGGGGCATGATCTTAATGCTGTGAGTATGCTGAG 404
QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
DB 405 CTCGAAGATCTGGAGAAACGATGATGATGATGATGATGATGATGATGATGATGATG 464

ORGANISM

Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Petunia.

REFERENCE

1 (bases 1 to 994)
Kramer, E.M. and Irish, V.F.
Evolution of the petal and seamen developmental programs: Evidence from comparative studies of the lower eudicots and basal angiosperms

AUTHORS

Int. J. Plant Sci. (2000) In press
2 (bases 1 to 994)
Kramer, E.M. and Irish, V.F.
Direct Submission

JOURNAL

Submitted (03-FEB-2000) MCB, Yale University, PO Box 208104, New Haven, CT 06511-8104, USA
location/Qualifiers

FEATURES

source
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SRDRLA"

CDS

ORIGIN

Alignment Scores:

Pred. No.: 5,38e-57 Length: 994
Score: 721.50 Matches: 142
Percent Similarity: 74.36% Conservative: 32
Best Local Similarity: 60.68% Mismatches: 49
Query Match: 59.33% Indels: 11
DB: Gaps: 4

US-10-069-527-4 (1-232) x AF230704 (1-994)

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QY 21 TySerLysArgArgAsnGlyIlePheLysIleSalGlnGluLeuThrValLeuCysAsp 40
DB 61 TACTCCAAAGAGAGAAATGGTTATTCAAGAAAGTAAAGAACTTACTGTTTGAT 120
QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlnTyrIleSerPro 60
DB 121 GCTAAGACTCTCTCATATGCTCTCCAGTACTAGGAATTCATGACTAATACCAAGTCC 180
QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTyr 80
DB 181 AACACTACGACAAATAAATGATGATTGTTACAGAGACACTGGGGTGGAATTTGG 240
QY 81 ArgThrHisGlnGluSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnAsnLys 100
DB 241 AACACGACTTACGAAATAATGCAAGAAATCTGAAACATGAAAGATATCAATACACAG 300
QY 101 LeuArgArgGlnIleArgGlnArgLeuGlnHisAspLeuAsnGlyLeuSerPheAspGlu 120
DB 301 CTAAAGAGAGAGATTAAGCAAGAACAGGGCAAGCAATGAGCGGCTCAATTTGACAGAA 360
QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
DB 361 TTGTGCACTTGCAGGGGAAAGCTCTGATCTCTAGCTGAATACGTGAAGAAAGATAT 420
QY 141 HisValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeuGlnGlnArg 160

DB

421 CATGTGATCAAGACTCAACAGATACCTTCAGAGAAAGGGTGAGAACTTAGAAGACGA 480

QY

161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaGlyGluAspProGlnTyr 180

DB

481 CATGAAAGCCCTGATCAT-----GATTGGAAAGCAAAAGGAGATCTCAACGTAT 531

QY

181 GlyTyrGluAspAsnGlnGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200

DB

532 GGTGTAGTGAATAATAGAGACATTTCAACTGCTATGCACTTTGCCAATGGGGTACAC 591

QY

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DB

592 AACCTTATGCTTTTGCTTCCACAGACGCTTCCACCCCAATCTTCAAAACGAGAGA---GGA 648

QY

219 LeuGlySerSerLysThrHisLeuHisAspLeuArgLeuAla 232

DB

649 TTGTGTTCT-----CGTGATCTACGCTTGCT 675

RESULT 6

AR372459

LOCUS AR372459 681 bp DNA linear PAT 12-SEP-2003

DEFINITION

Sequence 3 from patent US 6395892.

ACCESSION

AR372459

VERSION

AR372459.1 GI:34609786

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 681)
Strasburg, S.H., Rotmann, W., Brunner, A. and Sheppard, L.

AUTHORS

Floral homeotic genes for manipulation of flowering in poplar and other plant species

TITLE

Patent: US 6395892-A 3 28-MAY-2002;

JOURNAL

Location/Qualifiers

FEATURES

source
1..681
/organism="unknown"
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ORIGIN

US-10-069-527-4 (1-232) x AR372459 (1-681)

Alignment Scores:

Pred. No.: 4.26e-56 Length: 681
Score: 709.50 Matches: 149
Percent Similarity: 72.38% Conservative: 24
Best Local Similarity: 62.34% Mismatches: 45
Query Match: 58.35% Indels: 21
DB: Gaps: 5

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QY 21 TySerLysArgArgAsnGlyIlePheLysIleSalGlnGluLeuThrValLeuCysAsp 40
DB 61 TACTCCAAAGAGAGAAATGGTTATTCAAGAAAGTAAAGAACTTACTGTTTGAT 120
QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlnTyrIleSerPro 60
DB 121 GCTAAGACTCTCTCATATGCTCTCCAGTACTAGGAATTCATGACTAATACCAAGTCC 180
QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTyr 80
DB 181 AACACTACGACAAATAAATGATGATTGTTACAGAGACACTGGGGTGGAATTTGG 240
QY 81 ArgThrHisGlnGluSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnAsnLys 100
DB 241 AACACGACTTACGAAATAATGCAAGAAATCTGAAACATGAAAGATATCAATACACAG 300
QY 101 LeuArgArgGlnIleArgGlnArgLeuGlnHisAspLeuAsnGlyLeuSerPheAspGlu 120
DB 301 CTAAAGAGAGATTAAGCAAGAACAGGGCAAGCAATGAGCGGCTCAATTTGACAGAA 360

QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
 Db 361 CTGGCGCGCTCTTGACACATATGACTGAAGCCCTTGATGGTGGCTGGCAGAGATAC 420
 QY 141 HisValIleLysThrGlnThrGlnThrLysLysValLysAsnLeuGlnArg 160
 Db 421 CATGTGATCAAAACAAAAGAAAGAACTCAGAGAAAGAGTGAAGAAATTTAGAGAGAGA 480
 QY 161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGlnAlaIleGlyAspProGlnTyr 180
 Db 481 CATGAAACCTCTTGATGAGATAT-----GAAACCAAACTAGAGATGACAGATAT 531
 QY 181 GlyTyrGluAspAsnGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
 Db 532 GGTTAAGTGAACAT-----GAACTGCTGTGCACTTGCAAAATGGGGCTTCC 579
 QY 201 AsnLeuTyrThrPheHisLeuHis-----ProAsnLeu 212
 Db 580 AACCTCTATGATTCGCCCTGCATCAGGGCACAACCAACCAACCATCTCCCTAATCTT 639
 QY 213 HisHisGlyGlySerSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLeu 231
 Db 640 CACCTT---GGAGATGATTTGGAGCC-----CATGAACCTTCGCTT 678
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 AR372458 946 bp DNA linear PAT 12-SEP-2003
 LOCUS AR372458
 DEFINITION Sequence 2 from patent US 6395892.
 ACCESSION AR372458
 VERSION AR372458.1 GI:34609785
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 946)
 AUTHORS Strauss,S.H., Rottmann,W., Brunner,A. and Sheppard,L.
 TITLE Floral homeotic genes for manipulation of flowering in poplar and other plant species
 JOURNAL Patent: US 6395892-A 2 28-MAY-2002;
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 DEFINITION X60759
 ACCESSION X60759.1 GI:19385
 VERSION X60759.1
 KEYWORDS MADS box; TDR6 gene.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
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 1 (bases 1 to 895)
 Pnueli,L., Abu-Abaid,M., Zamir,D., Nacken,W., Schwarz-Sommer,Z. and Lifschitz,E.
 REFERENCE The MADS box gene family in tomato: temporal expression during floral development, conserved secondary structures and homology with homeotic genes from Antirrhinum and Arabidopsis
 JOURNAL Plant J. 1 (2), 255-266 (1991)
 MEDLINE 93251098
 PUBMED 1688249
 REFERENCES 2 (bases 1 to 895)
 Pnueli,L.
 DIRECT SUBMISSION
 JOURNAL Submitted (01-JUL-1991) L. Pnueli, Dept of Biology, Technion-Israel Inst of Technology, Haifa 32000, ISRAEL
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VERSION	AY098734.2	GI:24967131	
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REFERENCE	TITLE	JOURNAL	
AUTHORS	MEDLINE	PUBMED	
	22856390	13677468	
	2 (bases 1 to 945)	Buesi,M.V., D'Angelo,M.C. and Zabaleta,B.J. Direct Submission Submitted (22-AR-2002) Plant Molecular Biology, IIB-INTECH, Camino de la Estrella Vieja Chacabuco, RA 7110 Argentina	

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REFERENCE	3 (bases 1 to 945)
AUTHORS	Buší, M.V., D'Angelo, M.C. and Zabaleta, E.J.
TITLE	Direct Substitution
JOURNAL	Submitted (14-NOV-2002) Plant Molecular Biology, IIB-INTECH, Camino de Circunvalación de la Laguna Km6, Chacabuco, BA 7130, Argentina
REMARK	Sequence update by submitter
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; Cornales; Hydrangeaceae; Hydrangea.
 REFERENCE 1 (bases 1 to 939)
 AUTHORS Kramer, E.M. and Irish, V.F.
 TITLE Evolution of the petal and stamen developmental programs: Evidence from comparative studies of the lower eudicots and basal angiosperms
 JOURNAL Int. J. Plant Sci. (2000) In press
 REFERENCE 2 (bases 1 to 939)
 AUTHORS Kramer, E.M. and Irish, V.F.
 TITLE Direct Submission
 JOURNAL Submitted (03-FEB-2000) MDCB, Yale University, PO Box 208104, New Haven, CT 06511-8104, USA
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Petunia.
 REFERENCE 1 (bases 1 to 881)
 AUTHORS Kush, A., Brunelle, A., Shevell, D. and Chua, N.H.
 TITLE The cDNA sequence of two MADS box proteins in Petunia
 JOURNAL Plant Physiol. 102 (3), 1051-1052 (1993)
 MEDLINE 94105323
 PUBMED 8278527
 REFERENCE 2 (bases 1 to 881)
 AUTHORS Brunelle, A.N.
 TITLE Direct Submission
 JOURNAL Submitted (23-NOV-1992) A.N. Brunelle, The Rockefeller University,
 Dept of Plant Molecular Biology, 1230 York Avenue, New York, NY
 10021, USA
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 VERSION MADS-box protein.
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanales; Nicotiana.

REFERENCE
 AUTHORS Davies, B., Di Rosa, A., Eneva, T., Saedler, H. and Sommer, H.
 TITLE Combination of tobacco floral organ identity by expression of
 JOURNAL Plant J. 10 (4), 663-677 (1996)
 MEDLINE 97048712
 PUBMED 8893543
 REFERENCE 2 (bases 1 to 1113)
 AUTHORS Davies, B.
 TITLE Direct Submission

JOURNAL

Submitted (05-MAR-1996) B. Davies, MEIZ-KOELN, PLANT MOLECULAR
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CDS

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 Query Match: 52.47% Indels: 12
 DB: 8 Gaps: 5

ORIGIN

US-10-069-527-4 (1-232) x NTMADSBOX (1-1113)

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DEFINITION	S.tuberosum defA mRNA for deficiens analogue (clone pd4).				
ACCESSION	X67508				
VERSION	X67508.1 GI:511064				
KEYWORDS	defA gene; deficiens; MADS-box protein; transcriptional activator.				
SOURCE	Solanum tuberosum (potato)				
ORGANISM	Solanum tuberosum				
REFERENCE	Buhalata, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.				
AUTHORS	1 (bases 1 to 924)				
TITLE	Garcia-Maroto, F., Salamini, F. and Rohde, W.				
JOURNAL	Molecular cloning and expression patterns of three alleles of the Deficiens-homologous gene St-deficiens from Solanum tuberosum				
MEDLINE	Plant J. 4 (5), 771-780 (1993)				
FEATURES	94100991				
REFERENCE	2 (bases 1 to 924)				
AUTHORS	Maroto, Salamini and Rohde.				
JOURNAL	Unpublished				
AUTHORS	3 (bases 1 to 924)				
TITLE	Garcia-Maroto, F.				
JOURNAL	Direct Submission				
FEATURES	Submitted (24-AUG-1992) F. Garcia-Maroto, MPI f				
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REFERENCE 2 (bases 1 to 965)

AUTHORS Dunn, K.
 TITLE Direct Submission
 JOURNAL Submitted (05-MAR-1997) Biology, Boston College, Chestnut Hill, MA 02167, USA

COMMENT On Mar 5, 1997 this sequence version replaced gi:780292.
 FEATURES location/Qualifiers

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CDS

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US-10-069-527-4 (1-232) x ALFMBP (1-965)

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 Db 61 TACTCAAAACGAGAGATGCTCTTTTCAGAGAGCCATAGCTCACTGTTCTTTGAGAT 120
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 Db 361 CTGAGGCTTCTTGAAGATGAAATGACAGAGGCTCTCAAGCTATTCTGAGAGCGAAGTAT 420
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Db 421 AAGTGATTAACAATCAATTCAGATTGACACCCAAAGAAAGATTAAATATGAGAGAGAGGTC 480
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Search completed: September 26, 2004, 09:11:16
 Job time : 3968.76 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OW protein - nucleic search, using frame_plus_pzn model

Run on: September 26, 2004, 02:46:48 / Search time 389.781 Seconds
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Perfect score: 1216
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Searched: 337363 seqs, 212409041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	709.5	58.3	681	4	AA085393
3	709.5	58.3	946	4	AA085392
4	709.5	58.3	946	6	ABK88485
5	709.5	58.3	946	8	ACA62518
6	701.5	57.7	924	3	AA257943
7	641.5	52.8	882	2	AA051189
8	616.5	50.7	926	6	AA042259

9	585.5	48.1	969	3	AA055879	AA055879 Eucalyptu
10	569	46.8	959	3	AA040831	AA040831 Arabidops
11	564	46.4	954	3	AA051525	AA051525 Arabidops
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15	455.5	37.5	409	3	AA06790	AA06790 Eucalyptu
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19	419	34.5	386	3	AA057268	AA057268 Eucalyptu
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22	367	30.2	868	4	AA050103	AA050103 Gramy Sm
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ALIGNMENTS

RESULT 1	AA000104	AA000104 standard; cDNA; 982 BP.
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AC	AA000104	
XX	AA000104	
DT	11-SEP-2003	(revised)
DT	17-MAY-2001	(first entry)
XX		
DE	Granny Smith apple cDNA encoding MdAP3.	
XX		
KW	Granny Smith apple; MdAP3; seedless fruit; horticulture;	
KW	accelerated breeding programme; cross pollination; transgenic plant;	
KW	biennial bearing tendency; coding moth; ss.	
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OS	Malus x domestica; var. Granny Smith.	
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FT	Key	Location/Qualifiers
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XX		
PD	MO20011734-A1.	
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PD	15-MAR-2001.	
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PF	07-SEP-2000; 2000MO-NC000176.	
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PR	07-SEP-1999; 99NZ-00337688.	
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PA	(HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.	
XX		

PI Yao J, Morris BA;
XX WPI, 2001-235145/24.
DR P-PSDB; AAU00187.

XX New genetically modified fruiting plants that does not functionally
PT express MdPI or MdAP3 peptides, useful for producing seedless fruits,
PS specifically apple and its related species.

PS Claim 17; Fig 6; 41pp; English.

CC The sequence encodes Granny Smith apple MdAP3. The invention concerns a
CC fruiting plant that has been genetically modified so that it does not
CC functionally express the MdPI or MdAP3 peptide, producing seedless
CC fruits. The DNA constructs encoding non-functional variants of MdPI/MdAP3
CC may be used to transform fruiting plants, specifically apple and pear.
CC The polynucleotides may be used in modulating, reducing or eliminating
CC seed-bearing capacity in fruiting plants, used in horticulture, and in
CC breeding programmes to monitor the progress in breeding a stable seedless
CC fruiting plant. The polynucleotides may also be used in programmes for
CC identifying nucleic acid variants from fruiting plants. They can be used
CC for pre-selecting plants (mutated in MdPI, MdAP3 or their equivalents),
CC for use in an accelerated breeding programme to produce seedless fruit.
CC They may also be used in designing probes and primers for MdPI or MdAP3,
CC or their variants. The seedless fruiting plant is more convenient than
CC seeded fruit since these can be cropped without pollination, reducing
CC dependence on bees, pollinator varieties and warm weather at flowering.
CC The absence of pollen is also advantageous to alleviate environmental
CC concerns regarding the transfer of transgenes to non-transgenic by cross
CC pollination. Seedless cultivars can also avoid or reduce biennial bearing
CC tendencies that have been attributed to the inhibition of flower bud
CC formation by developing seeds and are less susceptible to codling moth
CC compared to seeded fruit. (Updated on 11-SEP-2003 to standardise OS
CC field)

XX Sequence 982 BP; 308 A; 203 C; 226 G; 245 T; 0 U; 0 Other;

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Pred. No.: 1,02e-121 Length: 982
Score: 1216.00 Matches: 232
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-069-527-4 (1-232) x AA00104 (1-982)

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DB 361 CTGGCTTCTTGAAGATGATGAGTGAAGTCTTCTTGAATGCCATACGTCAAGAAAGTAC 420
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QY 221 SerSerIlePheHisLeuHisAspLeuArgLeuAla 232
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RESULT 2

AAFS5393 standard; cDNA; 681 BP.

AAFS5393:

23-JUL-2001 (first entry)

Nucleotide sequence of the floral homeotic protein PTD.

Floral homeotic gene; PTD; PTF; PTA-1; PTA-2; floral tissue; LEAFY;

LEAFY; FLORICULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;

fertility; sterility; ss.

Populus balsamifera.

Key Location/Qualifiers

CDS 1..681

FT /tag= a

FT /product= "PTD"

CA2319853-A1.

01-APR-2001.

02-OCT-2000; 2000CA-02319853.

01-OCT-1999; 99US-00410464.

(UNIV-) UNIV OREGON HEALTH SCI.

Rottman WF, Strauss SH, Brunner AM, Sheppard LA;

WPI; 2001-336098/36.

P-PSDB; AAB68435.

Novel isolated polynucleotide derived from Populus species, useful for

producing transgenic plants having modified fertility characteristic,

particularly sterility.

Claim 25; Page 42-43; 69pp; English.

The present sequence encodes a floral homeotic protein, designated PTD. It is derived from Populus balsamifera subsp. trichocarpa. The floral homeotic proteins are expressed in floral tissues. PTF is a homologue of LEAFY (LFY) and FLORICULA (FLO), and is expressed in immature inflorescences on which floral primordia are developing. PTD is a homologue of DEFICIENS (DEF), and is strongly expressed in stamen primordia from the onset of organogenesis. PTA-1 and PTA-2 are homologues of AGAMOUS (AG). The floral homeotic proteins and

CC polynucleotides are useful for producing transgenic plants having
 CC modified fertility characteristics, particularly sterility
 XX
 SQ Sequence 681 BP, 228 A, 148 C, 157 G, 148 T, 0 U, 0 Other;

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Pred. No.:	3,356-67	Length:	681
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DB:	4	Gaps:	5

US-10-069-527-4 (1-232) x AAF85393 (1-681)

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QY 81 ArgThrHisGluGlnSerMetLysAspThrLeuTyrLysGluIleAsnAsnLys 100
DB 241 GGCACCTCATACGAAAGAAATGCAAGAGCCTTGAAGAGCGTGAATGATATCATCATAG 300
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QY 161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGlnAlaIleGlyLysAspProGlnTyr 180
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QY 181 GlyTyrGlnLysAspAsnGlnGlyAspTyrGlnUserAlaLeuAlaLeuSerAsnGlyAlaAsn 200
DB 531 GGTTTAGTGACAAAT-----GAACTGTGTTGACCTTGCAATGAGGCGCTTCC 579
QY 201 AsnLeuTyrThrPheHisLeuHisHis-----ProAsnLeu 212
DB 580 AACCTCTATGATTCGCGCTGATCAGCGGCAACACACACACACATCCTTATCTT 639
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RESULT 3

AAF85392
 ID AAF85392 standard; cDNA, 946 BP.

AAF85392;

23-JUL-2001 (first entry)

Nucleotide sequence of the floral homeotic protein PTD.

XX

KM Floral homeotic gene; PTD, PTF, PTA-G-1, PTA-G-2; floral tissue; LEAFY;
 KM LFY; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
 KM fertility; sterility; ss.

OS Populus balsamifera.

PH Key	Location/Qualifiers
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PN CA2319853-A1.

PD 01-APR-2001.

PF 02-OCT-2000; 2000CA-02319853.

PR 01-OCT-1999; 99US-00410464.

PA (YOR-) UNIV OREGON HEALTH SCI.

PI Rottman WH, Straus SH, Brunner AM, Shepard LA;

DR WPI: 2001-336098/36.

DX P-PSDB; AAB68435.

PT Novel isolated polynucleotide derived from Populus species, useful for
 PT producing transgenic plants having modified fertility characteristic,
 PT particularly sterility.

PS Claim 25; Page 41-42; 69pp; English.

XX The present sequence encodes a floral homeotic protein, designated PTD.
 CC It is derived from Populus balsamifera subsp. trichocarpa. The
 CC specification also describes PTF, PTA-G-1 and PTA-G-2 proteins. The floral
 CC homeotic proteins are expressed in floral tissues. PTF is a homologue of
 CC LEAFY (LFY) and FLORICAULA (FLO), and is expressed in immature
 CC inflorescences on which floral primordia are developing. PTD is a
 CC homologue of DEFICIENS (DEF), and is strongly expressed in stamen
 CC primordia from the onset of organogenesis. PTA-G-1 and PTA-G-2 are
 CC homologues of AGAMOUS (AG). The floral homeotic proteins and
 CC polynucleotides are useful for producing transgenic plants having
 CC modified fertility characteristics, particularly sterility

XX SQ Sequence 946 BP, 331 A, 184 C, 201 G, 230 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	5,176-67	Length:	946
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Percent Similarity:	72.38%	Conservative:	24
Best Local Similarity:	62.34%	Mismatches:	45
Query Match:	58.35%	Indels:	21
DB:	4	Gaps:	5

US-10-069-527-4 (1-232) x AAF85392 (1-946)

```

QY 1 MetAlaArgGlyLysIleGluIleLeuIleGluAsnGlnThrAsnArgGlnValThr 20
DB 1 ATGGGCTCGTGAAGAAATTGAATCAAGAGATCGAAACCCCAACAGGCAAGTCACC 60
QY 21 TyrSerLysArgArgAsnGlyIlePheLysIleGlnGlnGlnLeuThrValLeuCysAsp 40
DB 61 TACTCGAAGAGAGAAATGGATGTTTCAAGAAAGCCCAAGAACTCACTGACTTTGTGAT 120
QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
DB 121 GCTAAGGCTCTCTTATCATGTTCTCAACACTCAACAACTCAAGTCACTTACGCCCC 180
QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTyr 80
DB 181 TCCACATCGACAAAGAAATGATCATGATCATATCATCAAGAGCGTTAGGATGATCTGTGG 240
QY 81 ArgThrHisGluGlnSerMetLysAspThrLeuTyrLysLysGluIleAsnAsnLys 100

```

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Db 241 GGCACCTCAATACGAGAAATGCAAGAGCACTTGAGGAGAGCTGAATGATATCAATCATATAG 300
Qy 101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
Db 301 CTGAGACAAAGAAATAGGACAGAGAGAGAGAGGCGCTGAAATGATCTGAGCATTTGATCAT 360
Qy 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLeuTyr 140
Db 361 CTGCGCGGCTTGAGCAACATATATGCTGAACCTTGATGCTGCGTGGCAGAGAAATAC 420
Qy 141 HisValIleIleYThrGlnThrGluThrThrylsylsValysAsnLeuGluGlnArg 160
Db 421 CATGGATCAAAAACCAAAACCAAACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaIleArgGlyAspProGlnTyr 180
Db 481 CATGGAACCTCTTGATGAGATAT-----GAAACCAAAACTAGAGATTCGACAGTAT 531
Qy 181 GlyTyrGluAspAspAsnGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
Db 532 GATTTAGTGACAAAT-----GAAAGCTGCTGTGCACTTGCAAAATGGGGCTTCC 579
Qy 201 AsnLeuTyrThrPheHisLeuHisHis-----ProAsnLeu 212
Db 580 AACCTCATATGATTCGGCTGCTGATCAGGGGCAACACACACATCTCCATATCTT 639
Qy 213 HisHisGlyGlySerSerLeuGlySerSerLeuThrHisLeuHisAspLeuAlaGlu 231
Db 640 CACCTT---GGAGATGATTTGGAGCC-----CATGAACCTTCGCGCTT 678

RESULT 4
ABK88485
ID ABK88485 standard; cDNA; 946 BP.
XX
AC ABK88485;
XX
DT 29-AUG-2003 (revised)
DT 07-OCT-2002 (first entry)
XX
DE Poplar protein transduction domain, PTD, cDNA.
XX
KW Poplar; ss; gene; plant; DEFICIENS; transgenic; promoter;
KW protein transduction domain; floral homeotic gene;
KW floral-specific expression; cytotoxin; fertility; sterility; PTLF;
KW PTLF-1; PTLF-2.
XX
OS Populus balsamifera; subsp. trichocarpa.
XX
FH Key Location/Qualifiers
FT CDS 1..684
FT /*tag= a
FT /product= "PTD"
XX
PN US6395892-B1.
XX
PD 28-MAY-2002.
XX
PF 01-OCT-1999; 99US-00410464.
XX
PR 06-APR-1998; 98US-0080851P.
PR 06-APR-1999; 99US-00287700.
XX
FA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Straus SH, Rottmann W, Brunner A, Sheppard L;
XX
DR WPI; 2002-572853/61.
DR P-PDSB; ABG30865.
XX
PT New protein transduction domain promoter nucleic acid molecule useful for
PT producing transgenic plants having modified fertility characteristics,
PT particularly sterility.

```

```

XX
XX Example 1; Col 35-38; 46P; English.
XX
CC The invention relates to an isolated nucleic acid molecule especially a
CC protein transduction domain (PTD) promoter; (i) that hybridizes under
CC wash conditions of 0.2 x SSC (saline sodium citrate), 0.1 % SDS (sodium
CC dodecyl sulphate) at 65 plus or minus 5 degrees Celsius comprising 35
CC consecutive nucleotides of the PTD gene. PTD is a floral homeotic gene
CC and is the homologue of DEFICIENS. Also included are a recombinant
CC nucleic acid comprising the PTD promoter; a cell transformed with the
CC recombinant nucleic acid and a transgenic plant comprising the
CC expression of genes such as cytotoxins, that are employed in genetic
CC ablation strategies to produce trees having modified fertility
CC characteristics, including sterility. Genetic constructs comprising
CC antisense versions or dominant negative mutants of PTD are useful in
CC producing genetically engineered Poplar and other trees, and for sense
CC suppression. Also disclosed are 3 other homeotic genes PTLF, PTLF-1 and
CC PTLF-2 (none are defined). The present sequence is the PTD cDNA. (updated
CC on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 5,176-67 Length: 946
Score: 709.50 Matches: 149
Percent Similarity: 72.38% Conservative: 24
Best Local Similarity: 62.34% Mismatches: 45
Query Match: 58.35% Indels: 21
DB: Gaps: 5
XX
US-10-069-527-4 (1-232) x ABK88485 (1-946)
Qy 1 MetAlaArgGlyLysIleGluIleLeuLeuGlnGlnThrValThr 20
Db 1 ATGGGTCGTGGAAATGGAATGCAAGAGATCGAAAAACCCACAAACAGGCAAGTCAAC 60
Qy 21 TyrSerLysArgArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAsp 40
Db 61 TACTCGAAGAGAGAAATGCTATTTTTCAGAAAGCCAGAACTCATCTGTCTTGTGAT 120
Qy 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlyTyrTlleSerPro 60
Db 121 GCTAAGGCTCTCTTATCATATCTCTCCAACTCAACAACTCAATGATGATTAAGCCCC 180
Qy 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTyr 80
Db 181 TCCACATGACAAAGAAATCTACATCAATATCAAGACGTTAGGATGATGATCTGTGG 240
Qy 81 ArgThrHisGlnGluSerMetLysAspThrLeuTyrLysLeuGlyLeuIleAsnLys 100
Db 241 GGCACCTCAATACGAGAAATGCAAGAGCACTTGAGAGAGCTGATGATATCATATAG 300
Qy 101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
Db 301 CTGAGACAAAGAAATAGGACAGAGAGAGAGAGGCGCTGAAATGATCTGAGCATTTGATCAT 360
Qy 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLeuTyr 140
Db 361 CTGCGCGGCTTGAGCAACATATGACTGAAGCCTTGATGCTGCGTGGCAGAGAAATAC 420
Qy 141 HisValIleIleYThrGlnThrGluThrThrylsylsValysAsnLeuGluGlnArg 160
Db 421 CATGGATCAAAAACCAAAACCAAACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaIleArgGlyAspProGlnTyr 180
Db 481 CATGGAACCTCTTGATGAGATAT-----GAAACCAAAACTAGAGATTCGACAGTAT 531
Qy 181 GlyTyrGluAspAspAsnGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
Db 532 GATTTAGTGACAAAT-----GAAAGCTGCTGTGCACTTGCAAAATGGGGCTTCC 579

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QY	20	AsnLeuTyThrpheHisLeuHis	-----ProAsnLeu	21
Db	580	AAcCTTtAGCATTCcCGcCTGCATCAGGAGCAACACACACACATCTCCtTAACTT	-----	639
QY	213	HisHisGlyValSerSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLeu	221	
Db	640	CACCTT---GGAGATGATTTGGAGCC-----CATGAACCTTCGCCTT	678	
RESULT 5				
ID	ACA62518	standard; cDNA; 946 BP.		
XX	ACA62518;			
XX	18-AUG-2003	(first entry)		
DE	Poplar homeotic gene PTD, cDNA.			
KM	Poplar; ss; gene; PTD; deficiencies; homeotic gene; floral development;			
XX	sterile tree; pulp; paper; plant.			
OS	Populus balsamifera subsp. trichocarpa.			
XX				
TH	Key	Location/Qualifiers		
FT	CDS	1..684		
FT		/*tag= a		
FT		/product= "PTD"		
XX		/note= "This CDS is specifically claimed in claim 1"		
XX	US2003033628-A1.			
PD	13-FEB-2003.			
XX				
PF	21-MAR-2002; 2002US-00104580.			
XX				
PR	06-APR-1998; 98US-0080851P.			
PR	06-APR-1999; 99US-00287700.			
PR	01-OCT-1999; 99US-00410464.			
XX				
XX	(UYOR-) UNIV OREGON HEALTH SCI.			
PI	Strauss SH, Rottmann W, Brunner A, Shepard L;			
DR	WPI; 2003-466273/44.			
XX	P-PSDS; ABU61893.			
XX				
PT	New floral homeotic nucleic acid molecules, useful for the manipulation			
PT	of flowering in Poplar and other plant species, and for producing			
PT	transgenic plants having modified fertility characteristics, particularly			
PT	sterility.			
PS	Claim 1; Page 20-21; 48pp; English.			
XX				
CC	The invention relates to an isolated nucleic acid molecule comprising at			
CC	least 15 consecutive nucleotides of the gene, cDNA or coding sequence of			
CC	4 homeotic genes from poplar; PTLF (LEAFY and FLORICA homologue), PTD			
CC	(DEFILTEUS homologue), and PRAG-1/PRAG-2 (both homologues of AGAMOUS).			
CC	Also included are a recombinant nucleic acid molecule comprising a			
CC	promoter sequence operably linked to the nucleic acid molecule, a cell			
CC	transformed with the nucleic acid molecule, a transgenic plant comprising			
CC	the recombinant nucleic acid molecule and the purified proteins encoded			
CC	by the nucleic acids. The nucleic acid molecules are useful for the			
CC	manipulation of flowering in Poplar and other plant species, for			
CC	producing transgenic plants having modified fertility characteristics			
CC	(particularly sterility) and in the pulp and paper industries. The			
CC	present sequence is the poplar PTD cDNA			
XX				
SQ	Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;			
Alignment Scores:				
Pred. No.:	5,17e-67	Length:	946	
Score:	709.50	Matches:	149	
Percent Similarity:	72.38%	Conservative:	24	

[illegible]

FT Claim 1"

XX CA2227940-A1.

XX 06-OCT-1999.

XX 07-APR-1998; 98CA-02227940.

XX 06-APR-1998; 98US-00080851.

XX (UNIV-) UNIV OREGON HEALTH SCI.

XX Rottmann WH, Brunner AM, Shepard LA, Strauss SH.

XX WPI; 2000-106662/10.

XX P-PSDB; AAY58654.

XX Nucleic acid from *Populus trichocarpa* genes, useful for producing

XX transgenic plants, particularly trees, with modified fertility

XX characteristics such as sterility.

XX Claim 1; Page 46-47; 92pp; English.

XX The present sequence is that of cDNA encoding *Populus balsamifera* subsp.

XX *trichocarpa* PTD protein (see AAY58654). The PTD gene (see AA257942) is

XX of 4 newly identified floral homeotic genes from this poplar species. It

XX is a homologue of DBFL1ENS and is expressed strongly in stamen primordia

XX from the onset of organogenesis, and is also expressed at low levels in

XX carpel primordia. The invention provides nucleic acid sequences of these

XX 4 *Populus* genes, the corresponding cDNA sequences (see AA257942-49) and

XX deduced amino acid sequences (see AAY58454-57). It also provides methods

XX of using the gene and cDNA sequences to produce genetically engineered

XX *Populus* species and other trees having modified fertility

XX characteristics, including sterility. Genetic constructs useful in

XX producing genetically engineered *Populus* and other trees include

XX antisense versions of PTD, dominant negative mutants, and constructs

XX useful for sense suppression. Promoter sequences may be used to obtain

XX floral specific expression of genes such as cytochrome P450 genes

XX in genetic ablation strategies to produce trees having modified fertility

XX characteristics, including sterility. Sterile trees allow increased wood

XX yield and a reduction in the production of allergens such as pollen

XX

SQ Sequence 924 BP; 309 A; 185 C; 201 G; 229 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,676-66 Length: 924

Score: 701.50 Matches: 147

Percent Similarity: 72.38% Conservative: 26

Best Local Similarity: 61.51% Mismatches: 45

Query Match: 57.69% Indels: 21

DB: 3 Gaps: 5

US-10-069-527-4 (1-232) x AA257943 (1-924)

QY 1 MetAlaArgGlyLysIleGluIleLysLeuIleGluAsnGlnThrAsnArgGlnValThr 20

DB 1 ATGGGTCGTGGAAGATGAAATCAAGAAAGATGAAACCCCAAAACAGGCAAGTCAC 60

QY 21 TySerIysArgArgAsnGlyIlePheLysValAlaGlnGluLeuThrValLeuCysAsp 40

DB 61 TACCTGAAGAGAAAGATGATTTTCAAGAAAGCCCAAGACTCTGCTGCTTGTGAT 120

QY 41 AlaIysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlnTyrIleSerPro 60

DB 121 GCTAAGGTCTCTTATCATCTGCTCCCAACATCAACAACTCAATGATGATACCC 180

QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTrp 80

DB 181 TCCACATCGAAGAAAGATCTACGATCAATCAAGAAAGCTTTAGGCAATGCTGTG 240

QY 81 ArgThrHisGlnLysSerMetLysAspThrLeuTyrLysLeuLysIleAsnLys 100

DB 241 GGCAGCTCAATACGAAAGAAATGCAAGAGCACTTGAAGAGTGAATGATATCATATAG 300

QY 101 LeuArgAspGluIleArgGlnAArgGlnLysAspLeuAsnGlyLeuSerPheAspGlu 120

DB 301 CTGAGCAAGAAATAGGCAAGAGAGAGAGAGGCGCTGAAATGATCTAGACATGATAT 360

QY 121 LeuAlaSerLeuAspAspGluMetGlnSerLeuAspAlaIleArgGlnArgLysTyr 140

DB 361 CTGCGCGGCTTGACCAACATATGACTGACCACTGATGCTGCGCGGCAAGAGATAC 420

QY 141 HisValIleLysThrGlnThrGluThrThrLysLysLysValLysAsnLeuGlnArg 160

DB 421 CATGATATCAAGCAAGAAAGCTTACAGAAAGAGAGAGATTTAGAGAGAGGA 480

QY 161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGlnAlaIleArgGlnAspProGlnTyr 180

DB 481 CATGAAACCTCTTATGATGAAATAT-----GAAAGCAAACTAGAGATGACAGTAT 531

QY 181 GlyTyrGlnAspAsnGluGlyAspTyrGlnSerLalaLeuAlaLeuSerAsnGlyAlaAsn 200

DB 532 GGTTAGTGAGCAAT-----GAACTGCTGTGACATTGCAATGAGGCTTCC 579

QY 201 AsnLeuTyrThrPheHisLeuHisHis-----ProAsnLeu 212

DB 580 AACCTCTATGATTCGCTGCTGATTCAGGCAACACCAACCAACATCTCCCTATCTT 639

QY 213 HisHisGlyGlySerSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLeu 231

DB 640 CACCTT---GGAGATGATTTGGAGCC-----CATGAACCTTGCCCTT 678

RESULT 7

ID AA051189

XX AA051189 standard; DNA; 882 BP.

XX

XX AA051189;

XX

XX 25-MAR-2003 (revised)

XX 19-JUN-1994 (first entry)

XX

XX Homeotic gene green petal.

XX

XX Plant; organ morphogenesis; control; petunia; petals; ss.

XX

XX Petunia.

XX

XX Key location/Qualifiers

XX FT 17.713

XX CDS /tag= a

XX

XX W09321322-A1.

XX

XX 28-OCT-1993.

XX

XX 13-APR-1993; 93WO-US003508.

XX

XX 13-APR-1992; 92US-00867580.

XX

XX 06-JUL-1992; 92US-00909589.

XX

XX (UNIV) UNIV ROCKEFELLER.

XX

XX Halfter U, Van Der Krol AR, Kush A, Chua N;

XX

XX WPI; 1993-351732/44.

XX

XX P-PSDB; AAR43385.

XX

XX Plant organ morphogenesis control and determ. - by regulating the

XX expression of homeotic genes which determine the identity of the organ.

XX

XX Claim 13; Fig 2; 74pp; English.

XX

XX The homeotic gene green petal from petunia has been cloned and

XX characterised previously. The gene was used in a new method for

XX controlling the morphogenesis of plant organs comprising regulating the

XX expression of the gene using ectopic expression. Such a method can be

CC used to determine and control plant organ morphogenesis, such as
 CC modifying petals without altering the reproductive portions of the
 CC flower. See also A051190-1. (updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 882 BP, 306 A, 155 C, 182 G, 239 T, 0 U, 0 Other;

Alignment Scores:
 Pred. No.: 1,056-59 Length: 882
 Score: 641.50 Matches: 129
 Percent Similarity: 71.12% Conservative: 36
 Best Local Similarity: 55.60% Mismatches: 52
 Query Match: 52.75% Indels: 15
 DB: 2 Gaps: 4

US-10-069-527-4 (1-232) x A051189 (1-882)

QY 1 MetAlaArgGlyLeuIleGluIleLeuIleGluAlaGlnIleThrAsnArgGlnValThr 20
 DB 18 ATGGCTCGTGAAGATCCAGATCAAGAAATGAGAAACCAACCAAGCCAGTGAACA 77
 QY 21 TysSerLysArgArgAsnGlyIlePhePheLysValAlaGlnIleLeuThrValLeuCysAsp 40
 DB 78 TTTTCTAAGAGAAAGAAATGACTTTTCAAGAAAGCTAATGAACTCACTGTTCTTGTGAT 137
 QY 41 AlAlaValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlyTyrIleSerPro 60
 DB 138 GCCAAGATTCATATGATTTGATTTCCAGTCTGCAAGCTTCAAGATTCATATGATTCACA 197
 QY 61 Thr 80
 DB 196 TTTATCAGACTAAGAGATGTTGATTCATCTGTCACAAAGACTGTTGAGATGATTTGG 257
 QY 81 ArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnAsnLys 100
 DB 258 AACGCCCATATGAGAAATGCAAGAGCACTGAGAGAAAGCTAAAGAAATGAAATGCAAT 317
 QY 101 LeuAlaArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspLeu 120
 DB 318 CTCGCAAAAGAGATGAGGAGAGATGGAGAAAGCTTAAAGATCTTAAGATGAGAGAG 377
 QY 121 LeuAlaSerLeuAspArgLysMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
 DB 378 TTGGAAGAGCTATGAGAAATGTCACAAATTTCTTCAAGCTTATTCGGAAGAAAGATAT 437
 QY 141 HisValIleLysThrGlnThrGlnThrThrLysLysValLysValLysAsnLeuGlnArg 160
 DB 438 AAGGTGATTTGCAATCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 497
 QY 161 ArgGlyAsnMetLeuHisGlyTyrPheAspArgGlnIleAlaGlyLysAspProGlnTyr 180
 DB 498 CATAGGATCTCTTCT 545
 QY 181 GlyTyrGluAspAsnGluLysArgTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
 DB 546 GGGCTAGTGAACAAGAGAGTGAACAATCTGTGCTTGGTTTCCAAATGAGAGGAT 605
 QY 201 AsnLeuTyrThrPheHisLeu-----HisHisProAsnLeu 212
 DB 606 GGCATATTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCTTAAGCT 665
 QY 213 HisHisGlyLysSerSerLeuGlySerSerIleThr 224
 DB 666 CACAGTGGTGA-----GGCTCTGATATCACT 692
 RESULT 8
 ID AAD42259 standard; cDNA, 926 BP.
 AC AAD42259;
 AC AAD42259;
 AC AAD42259;
 DT 04-NOV-2002 (first entry)
 XX

DE Soybean AP3 homologue cDNA from clone sflin.pk001.116.
 XX
 KW Floral developmental protein; flowering locus T; APTALA3; transgenic;
 KW FT; AP3; transgenic plant; fertility; flower development; gene mapping;
 KW sterility; plant growth; inflorescence architecture; plant morphology;
 KW tissue culture; cell division; soybean; gene; ss.
 XX
 OS Glycine max.
 XX
 FH Key Location/Qualifiers
 FT CDS 11..694
 FT /tag= a
 FT /product= "Soybean AP3 homologue protein"
 XX
 PN W0200244390-A2.
 XX
 PD 06-JUN-2002.
 XX
 XX 21-NOV-2001; 2001WO-US043750.
 XX
 XX 28-NOV-2000; 2000US-0253415P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX
 PI Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;
 DR WPI; 2002-547703/58.
 DR P-PSDB; AAE25757.
 XX
 PT New floral developmental polypeptide having flowering locus T or Ap3
 PT homolog activity, useful for immunological screening of cDNA expression
 PT libraries.
 XX
 PS Claim 6; Page 80; 88pp; English.
 XX
 CC The present invention relates to novel floral developmental proteins,
 CC more specifically flowering locus T (FT) or APTALA3 (AP3) homologue
 CC proteins and polynucleotides encoding such proteins. Floral developmental
 CC polynucleotides are useful for transforming cells or for producing plants
 CC by transforming the plant cells with the polynucleotides and regenerating
 CC the plants from the transformed plant cells. Sequences of the invention
 CC are useful for immunological screening of cDNA expression libraries. They
 CC are also useful for creating transgenic plants. Polynucleotides of the
 CC invention are used as probes for genetically and physically mapping the
 CC genes that they are a part of and as markers for traits linked to those
 CC genes. AP3 homologues may be useful for engineering plant sterility or
 CC fertility, flower development and morphology. FT or FTd homologues are
 CC useful for engineering flowering time, plant growth rate, inflorescence
 CC architecture, tissue culture morphology and rate of cell division to
 CC enhance transformation. The present sequence is soybean AP3 homologue
 CC cDNA
 XX
 SQ Sequence 926 BP, 304 A, 195 C, 194 G, 233 T, 0 U, 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 5,626-57 Length: 926
 Score: 616.50 Matches: 118
 Percent Similarity: 70.35% Conservative: 41
 Best Local Similarity: 52.21% Mismatches: 60
 Query Match: 50.70% Indels: 7
 DB: 6 Gaps: 3
 US-10-069-527-4 (1-232) x AAD42259 (1-926)
 QY 1 MetAlaArgGlyLysIleGluIleLeuIleGluAlaGlnIleThrAsnArgGlnValThr 20
 DB 11 ATGGCTAGAGAAAGATCCAGATCAAGATGAGAAACCAACCAAGCCAGTGAACA 70
 QY 21 TysSerLysArgArgAsnGlyIlePhePheLysValAlaGlnIleLeuThrValLeuCysAsp 40
 DB 71 TACTCTAAGAGAGAGATGCTTTTCAAGAAAGCTAATGAACTCACTGTTCTTGTGAT 130
 QY 41 AlAlaValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlyTyrIleSerPro 60


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PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149928P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151066P.
PR 30-AUG-1999; 99US-0151080P.
PR 31-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

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Alignment Scores:

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Pred. No.: 7.99e-52
Score: 569.00
Percent Similarity: 67.29%
Best Local Similarity: 53.27%
Query Match: 46.79%
DB: 3

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US-10-069-527-4 (1-232) x AAC40831 (1-959)

```

Length: 959
Matches: 114
Conservative: 30
Mismatches: 66
Indels: 4
Gaps: 2

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DB 564 GCACTAGTAGACAAATGAGAGATTCAGACTCTTGGATTCCAATCGAAGAGGTCA 623
QY 201 AsnLeuTyrThrPheHisLeuHisHisProAsnLeuHis 214
DB 624 CGTGCTTAGCGCTCTTCGTTCCACAG--AACCATCAGCAG 662

RESULT 11
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XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 68842.
XX KM Hybridisation assay; genetic mapping; gene expression control;
XX KM protein identification; signal transduction pathway; metabolic pathway;
XX KM promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
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 DT 04-NOV-2002 (first entry)
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 DE Corn AP3 homologue cDNA from clone ctain.PK050.48.
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 KW Floral developmental protein; flowering locus T; APETALA3; transgenic;
 KW FT; AP3; transgenic plant; fertility; flower development; gene mapping;
 KW sterility; plant growth; inflorescence architecture; plant morphology;
 KW tissue culture; cell division; corn; gene; ss.
 XX
 OS Zea mays.
 XX
 FH Key Location/Qualifiers
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 PD 06-JUN-2002.

PF 21-NOV-2001; 2001W0-US043750.
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 PI Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;
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 DR MPI: 2002-547703/58.
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 P-PSDB; AAE25755.
 PT New floral developmental polypeptide having flowering locus T or Ap3
 PT homolog activity, useful for immunological screening of cDNA expression
 PT libraries.
 PS
 XX
 XX Claim 6; Page 77-78; 88pp; English.
 CC The present invention relates to novel floral developmental proteins,
 CC more specifically flowering locus T (FT) or APETALA3 (AP3) homologue
 CC proteins and polynucleotides encoding such proteins. Floral developmental
 CC polynucleotides are useful for transforming cells or for producing plants
 CC by transforming the plant cells with the polynucleotides and regenerating
 CC the plants from the transformed plant cells. Sequences of the invention
 CC are useful for immunological screening of cDNA expression libraries. They
 CC are also useful for creating transgenic plants. Polynucleotides of the
 CC invention are used as probes for genetically and physically mapping the
 CC genes that they are a part of and as markers for traits linked to those
 CC genes. AP3 homologues may be useful for engineering plant sterility or
 CC fertility, flower development and morphology. FT or TFL homologues are
 CC useful for engineering flowering time, plant growth rate, inflorescence
 CC architecture, tissue culture morphology and rate of cell division to
 CC enhance transformation. The present sequence is corn AP3 homologue cDNA
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 SQ Sequence 1257 BP; 320 A; 353 C; 340 G; 244 T; 0 U; 0 Other;
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 Score: 553.50 Matches: 122
 Percent Similarity: 64.65% Conservative: 33
 Best Local Similarity: 51.05% Mismatches: 63
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Best Local Similarity: 52.09%
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US-10-069-527-4 (1-232) x AAC40685 (1-954)

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25-JAN-2001 (first entry)

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homeodomain zipper; LIM domain; AP2; ERBBs; zinc finger domain;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: September 26, 2004, 05:39:13 ; Search time 72.1432 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	709.5	58.3	946	4	US-09-410-464-2
3	419.5	34.5	4285	4	US-09-410-464-1
4	296	24.3	945	2	US-08-485-981-9
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6	295	24.3	1059	2	US-08-867-087B-14
7	287	23.6	1180	2	US-08-867-087B-16
8	285	23.4	798	4	US-09-611-659A-3
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ALIGNMENTS

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US-09-410-464-3
Sequence 3, Application US/09410464
Patent No. 6395892
GENERAL INFORMATION:
APPLICANT: Straus et al.
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
FILE REFERENCE: 53375
CURRENT APPLICATION NUMBER: US/09/410,464
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: 09/287,700
EARLIER FILING DATE: 1999-04-06
EARLIER APPLICATION NUMBER: 60/080,851
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 681
TYPE: DNA
ORGANISM: Populus balsamifera subsp. trichocarpa
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(681)
US-09-410-464-3

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Pred. No.: 8.65e-79
Score: 709.50
Percent Similarity: 72.38%
Best local Similarity: 62.34%
Query Match: 58.35%
DB: 4
Gaps: 5
Length: 681
Matches: 149
Conservative: 24
Indels: 45
Mismatches: 21

US-10-069-527-4 (1-232) x US-09-410-464-3 (1-681)

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/ GENERAL INFORMATION:
/ APPLICANT: Strauss et al.
/ TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
/ FILE REFERENCE: 53375
/ CURRENT APPLICATION NUMBER: US/09/410,464
/ CURRENT FILING DATE: 1999-10-01
/ EARLIER APPLICATION NUMBER: 09/287,700
/ EARLIER FILING DATE: 1999-04-06
/ EARLIER APPLICATION NUMBER: 60/080,851
/ EARLIER FILING DATE: 1998-04-06
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.0
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/ TYPE: DNA
/ ORGANISM: Populus balsamifera subsp. trichocarpa
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(684)
/ US-09-410-464-2

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DB	532	GGTTTAGTGAACAT-----GAACTGCTGTGCACTTGCAATGGGGCTTCC	579
QY	201	AsnLeuTyrThrPheHisPheHisHis-----ProAsnLeu	212
DB	580	AACCTTAGCATTCGGCTGTGATACGGGCAACCAACCAACCACTTCCCTAATCTT	639
QY	213	HisHisGlyLysSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLeu	231
DB	640	CACCTT---GAGATGATTTGGAGCC-----CATGAACCTTCGCTT	678

RESULT 3
US-09-410-464-1
Sequence 1, Application US/09410464
Patent No. 6395892
GENERAL INFORMATION:
APPLICANT: Straus et al.
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
FILE REFERENCE: 53375
CURRENT APPLICATION NUMBER: US/09/410.464
EARLIER FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: 09/287,700
EARLIER FILING DATE: 1999-04-06
EARLIER APPLICATION NUMBER: 60/080,851

EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 1
LENGTH: 4285
TYPE: DNA
ORGANISM: *Populus balsamifera* subsp. *trichocarpa*
US-09-410-464-1

Alignment Scores:
Pred. No.: 1.37e-41 Length: 4285
Score: 419.50 Matches: 150
Percent Similarity: 29.26% Conservative: 25
Best Local Similarity: 25.08% Mismatches: 46
Query Match: 34.50% Indels: 379
DB: 4 Gaps: 12

US-10-069-527-4 (1-232) x US-09-410-464-1 (1-4285)

QY 1 MetAlaArGgLyLeuIleGluIleuLeuSerLeuLeuGluSerLeuValThr 20
DB 2001 ATGGGTGGTGAAGATTGTAATCAAGAAAGATCGAAAGCCCAAGCAAGGAGTCAAC 2060
QY 21 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 40
DB 2061 TACTGGAAG 2120
QY 41 AAlaValSerLeuIleuLeuSerLeuLeuSerLeuLeuSerLeuValThr 60
DB 2121 GCTAAGGTCCTCTTATCATGTTCTCCAAACACTCAACAACTCAAGATGATGATGATG 2180
QY 61 ThrThrThr----- 63
DB 2181 TCCACATGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2240
QY 63 ----- 63
DB 2241 TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2300
QY 64 -----ThrLeuSerLeuLeuSerLeuLeuSerLeuValThr 74
DB 2301 GATGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2360
QY 74 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 85
DB 2361 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2420
QY 85 ----- 85
DB 2421 CTAATGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2480
QY 86 -----SerLeuLeuSerLeuLeuSerLeuLeuSerLeuValThr 104
DB 2481 GCAGAAATGCAAGAGCACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2540
QY 104 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 105
DB 2541 AATTCAGTACTTCAAAAGAAATTAACCTTCGATATGATGATGATGATGATGATGATG 2600
QY 106 -----ArgLeuLeu 109
DB 2601 GGAATATCTGTAATTTTGGAGCTACTATTAAGTATTTGTTTAAAGGCGAGAGAGA 2660
QY 109 GAGGAG 129
DB 2661 GAGGAG 2720
QY 129 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 139
DB 2721 CTGAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2779
QY 139 ----- 139

DB 2780 ATATATATCAAGTCTATCTATCTTAAATTTGAGCTACTAGTATTTGATGCGTCC 2839
QY 139 ----- 139
DB 2840 GGTGATCAAGAGGATTAATCTAGATCTAGTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2899
QY 139 ----- 139
DB 2900 TGAAGATTTTAAATAAATAATGATTTTGAATCACTATTAACATTCATCATCT 2959
QY 139 ----- 139
DB 2960 ACAATCGAATCTTACATTTATCAAACTTCAATAGATCTTATATATATATATTA 3019
QY 139 ----- 139
DB 3020 CCGGTGGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3079
QY 139 ----- 139
DB 3080 TTTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3139
QY 139 ----- 139
DB 3140 ACCGTGTTAGAAAGAAATATACACACCTTGAACCTTGTCTTCTTCTTCTTCTTCTTCT 3199
QY 139 ----- 139
DB 3200 GATTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3259
QY 140 -----ThrLeuVal 143
DB 3260 GATATTAACACTTACACTTACACTTACACTTACACTTACACTTACACTTACACTTACACT 3319
QY 143 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 153
DB 3320 TCAAAACCAAAAG 3379
QY 154 -----ValLeu 156
DB 3380 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3439
QY 156 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 165
DB 3440 ATTTAG 3499
QY 166 -----HisGly 169
DB 3500 GCTTGTGTTGCTAATTTTCCAACTTGAAGAAACATGATTAACCTGAGATTTTCTT 3559
QY 169 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 183
DB 3560 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3618
QY 183 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 203
DB 3619 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3666
QY 203 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 215
DB 3667 ATGATTTCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3725
QY 215 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 231
DB 3726 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3758

RESULT 4
US-08-485-981-9
Sequence 9, Application US/08485981
Patent No. 5861542
GENERAL INFORMATION:
APPLICANT: An. Gynheung
TITLE OF INVENTION: GENE CONTROLLING FLORAL DEVELOPMENT AND

TITLE OF INVENTION: APICAL DOMINANCE IN PLANTS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESS: Klarquist Sparkman Campbell Leigh &
 ADDRESSEE: Whinston
 STREET: One World Trade Center
 STREET: 121 S.W. Salmon Street
 STREET: Suite 1600
 CITY: Portland
 STATE: Oregon
 COUNTRY: United States of America
 ZIP: 97204
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disk, 3-1/2 inch
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/485,981
 FILING DATE: June 7, 1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/323,449
 FILING DATE: October 14, 1994
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Alan. E.
 REGISTRATION NUMBER: 35,123
 REFERENCE/DOCKET NUMBER: 4630-42933
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (503) 226-7391
 TELEFAX: (503) 228-9446
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 945 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double stranded
 TOPOLOGY: linear
 US-08-485-981-9

Alignment Scores:
 Pred. No.: 3,04e-27 Length: 945
 Score: 296.00 Matches: 77
 Percent Similarity: 53.33% Conservative: 35
 Best Local Similarity: 36.67% Mismatches: 68
 Query Match: 24.34% Indels: 30
 Gaps: 6

US-10-069-527-4 (1-232) x US-08-485-981-9 (1-945)

QY 1 Metlaarqgllyslleqlllelyleuileqllasnglnthrasnaarqglvaltnr 20
 Db 16 ATGGGAAGGGGTAGGGTGAAGCTTAAGAAATAGAGAACAGATCAACAGCAAGTGAAC 75
 QY 21 TyserlysaarqarqanqlylePhelyslysalaglnqluleuthrvalleucysasp 40
 Db 76 TTCCCTAAGAGAAATGACCTTTGAAAAAGCTTATAGCTTTGTCTTTGTGAT 135
 QY 41 Alalyvalserleuilemetleuserasnthrasnlysechisgluyrileserpro 60
 Db 136 GCTAGAGGTGCTCATCATCTTCTCCAAATAGGGGAAACGTAACGAGTCTCAGTAGC 195
 QY 61 ThthrhrthrlyssarsetlyrAspaaptyrGlnlys-----Thr 74
 Db 196 TCTAGCATGCTCAAGACATTA--GAGAGGTACCAAGAGCAACAAAGATCTTGAAGCTT 252
 QY 75 Metgyllyleaspleutparqthrhsglglusermetlysaapthrlleutplysleu 94
 Db 253 ACCAATATATCCACACAGAGCACTGGAATAATAGTCAACAAGATATCTTGAAGCTT 312
 QY 95 lyeqlulileasnaenlyslleuargarglulilearglnlrgleuglyhsaapleuaen 114
 Db 313 AAAGCAGCTTACGAGGATTAACGAGATCAACAGAAATCTTCTGTGTAAGATCTTGCG 372

QY 115 GlyleuserPheaspGluLeuAlaserleuasepajumetGlnserSerleuaspala 134
 Db 373 CCTTGAATATGCAAGAACTTGAATCACTTGAAGAGCACTGATATGTCACCTGAACAG 432
 QY 135 lleaarg-----Glnarglystyr 140
 Db 433 ATTGCATCAACTCGACATCACTTAATGTTGATCACTTACAGATCTTCAAGAAAGAA 492
 QY 141 Hisvalilleysthrlthrlthrlthrlthrlthrlthrlthrlthrlthrlthrlth 160
 Db 493 CATGCATTAAACGAAGCAACGAACCTTGAACCAAGCTTG-----ATG 537
 QY 161 ArgglvaenmetleuilegilytyrPheaspGlnqlualalaglygluaspproclntyr 180
 Db 538 GAAGAGGCAACTTAATCTGCAGTGGCAACAAATGCA-----CAAGATATGGGCTAC 591
 QY 181 GlytyrGlu-----AspaangluGlyasp 188
 Db 592 GGCGGCAAAACAATCAATCAAGGGCGAT 621

RESULT 5
 US-08-867-087B-10
 Sequence 10, Application US/08867087B
 Patent No. 5990386
 GENERAL INFORMATION:
 APPLICANT: An. Gynheung
 TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
 NUMBER OF SEQUENCES: 70
 CORRESPONDENCE ADDRESS:
 ADDRESS: Klarquist Sparkman Campbell Leigh &
 ADDRESSEE: Whinston, LLP
 STREET: One World Trade Center
 STREET: 121 S.W. Salmon Street
 STREET: Suite 1600
 CITY: Portland
 STATE: Oregon
 COUNTRY: United States of America
 ZIP: 97204
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disk, 3-1/2 inch
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/867,087B
 FILING DATE: June 2, 1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.S. 08/323,449
 FILING DATE: October 14, 1994
 APPLICATION NUMBER: U.S. 08/485,981
 FILING DATE: June 7, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Alan. E.
 REGISTRATION NUMBER: 35,123
 REFERENCE/DOCKET NUMBER: 4630-47071
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (503) 226-7391
 TELEFAX: (503) 228-9446
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 945 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double stranded
 TOPOLOGY: linear
 US-08-867-087B-10

Alignment Scores:
 Pred. No.: 3,04e-27 Length: 945
 Score: 296.00 Matches: 77
 Percent Similarity: 53.33% Conservative: 35

Best Local Similarity: 36.67% Mismatches: 68
 Query Match: 24.34% Indels: 30
 DB: 2 Gaps: 6

US-10-069-527-4 (1-232) x US-08-867-087B-10 (1-945)

QY 1 MetAlaArgGlyLysIleGluIleuLeuIleGluLeuGlnThrAsnArgIleValThr 20
 DB 16 ATGGAGAGGGGTGAGGTTGAGCTTGAAGATAGAGAACAGATCAACAGGCAAGTGAAC 75
 QY 21 TyrSerLysArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAsp 40
 DB 76 TTCGCTAAGAGAGAAATGAGACTTTGAAAAAGCTTATGAGCTTTCGTTCTTGTCAT 135
 QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHsGluTyrIleSerPro 60
 DB 136 GCTGAGGTTGCTCATCATCTTCTCCAAATAGGGGAAAACTGATGAGTCTGAGTGAAC 195
 QY 61 ThrThrThrThrLysSerMetCysAspTyrArgIleLys-----Thr 74
 DB 196 TCTACAGAGCTCAAGACATTA---GAGAGGTACCAAGAGTGCACACTACGAGCACAGAG 252
 QY 75 MetGlyIleAspLeuTyrPArgThrHsGluGlnSerMetLysAspThrLeuTyrLysLeu 94
 DB 253 ACCAATATATCCACAGAGAGAGCACTGGAAATATAGTACCAACAGAAATACCTGAAGCTT 312
 QY 95 LysGluIleAsnAsnLysLeuArgArgIleIleArgIleGlnArgLysIleAsn 114
 DB 313 AAAGACGCTTACGAGCATTAACGAGATCAACAGAAATCTTCTTGGAAGATCTTGAC 372
 QY 115 GlyLeuSerPheAspGluLeuLysSerLeuAspAspGlnMetGlnSerSerLeuAspAla 134
 DB 373 CCTTGATAGCAAGAACTTGAATCATCTTGAGAGCAGCTTGATATGCTGCTGAAAG 432
 QY 135 IleArg-----GlnArgLysTyr 140
 DB 433 ATTCATCACTACGAGACTCACTTAATGTGATCACTTACAGATCTTCAAGAGAAAGAA 492
 QY 141 HisValIleLysThrGlnThrGlnThrLysLysValLysValLysAsnLeuGlnLysArg 160
 DB 493 CATGCACTTAACGAGAAACAGAACTTGAACAAAGCTTG-----ATG 537
 QY 161 ArgGlyAsnMetLeuHsIleGlyTyrPheAspGlnGlnAlaLysGluAspProGlnTyr 180
 DB 538 GAAGAGAGCACTAATCTGACGTGGCAACAAATGCA-----CAAGATATGGGTAC 591
 QY 181 GlyTyrGlu-----AspAsnGluLysAsp 188
 DB 592 GGCCGGCAAACTCAAACTCAGGGCGCAT 621

RESULT 6
 US-08-867-087B-14
 Sequence 14, Application US/08867087B
 Patent No. 5990386
 GENERAL INFORMATION:
 APPLICANT: An, Gynheung
 TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
 TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
 NUMBER OF SEQUENCES: 70
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kiarquist Sparkman Campbell Leigh &
 ADDRESSEE: Whitson, LLP
 STREET: One World Trade Center
 STREET: 121 S.W. Salmon Street
 CITY: Portland
 STATE: Oregon
 COUNTRY: United States of America
 ZIP: 97204
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disk, 3-1/2 inch
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS DOS

SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/867,087B
 FILING DATE: June 2, 1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: U.S. 08/323,449
 FILING DATE: October 14, 1994
 APPLICATION NUMBER: U.S. 08/485,981
 FILING DATE: June 7, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Dow, Alan, E.
 REGISTRATION NUMBER: 35,123
 REFERENCE/DOCKET NUMBER: 4630-47071
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (503) 226-7391
 TELEFAX: (503) 228-9446
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1059 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double stranded
 TOPOLOGY: linear

Alignment Scores:

Pred. No.: 4.8e-27 Length: 1059
 Score: 295.00 Matches: 83
 Percent Similarity: 49.40% Conservative: 41
 Best Local Similarity: 33.07% Mismatches: 71
 Query Match: 24.26% Indels: 56
 DB: 2 Gaps: 9

US-10-069-527-4 (1-232) x US-08-867-087B-14 (1-1059)

QY 1 MetAlaArgGlyLysIleGluIleuLeuIleGluLeuGlnThrAsnArgIleValThr 20
 DB 98 ATGGAGAGGGGTGAGGTTGAGCTTGAAGATAGAGAACAGATCAACGGAAGGTGACG 157
 QY 21 TyrSerLysArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAsp 40
 DB 158 TTCGCTAAGAGAGAAATGAGACTTTGAAAAAGCTTATGAGCTTTCGTTCTTGTCAT 217
 QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHsGluTyrIleSerPro 60
 DB 218 GCCGAGTCCGCTCATCATCTTCTCCAAACGGCGCAAGCTTACGAGTCTGACGACC 277
 QY 61 ThrThrThrThrLysSerMetCysAspTyrArgIleLysThr-----MetGlyIleAsp 78
 DB 278 CAGGCACTGACTTAACGCTT---GAGAGATACAGAAATGCACTTACGAGAGACCGGAA 334
 QY 79 LeuTyrPArgThrHsGlnGlnSer-----MetLysAspThrLeuTyrLys 93
 DB 335 ACAGCTGTCCAAATAAGAGAAAGTGAAGCAATGAAAGCTAGCCGCAATGAACTCAAA 394
 QY 94 LeuLysGluIleAsnAsnLysLeuArgArgIleIleArgIleGlnArgLysIleAsnLeu 113
 DB 395 CTGAGAGCAAGGTTGAAAAATTAACAGGACTCAAGAAATTTGCTGGGTTCAGATCTT 454
 QY 114 AsnGlyLeuSerPheAspGluLeuLysSerLeuAspAspGlnMetGlnSerSerLeuAsp 133
 DB 455 GATTCATTTAGGCATTAAGAGAGCTGAGAGCTTGAAGAGAGAGCTGATTCCTCTGAAG 514
 QY 134 AlaIleArg-----GlnArgLys 139
 DB 515 CACGTCAGAACTACAGAGCAAAACATCTGTCAGACCACTGACGAGCTTCAAGAGAAAG 574
 QY 140 TyrHisValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeuGlnLys 159
 DB 575 GAACAATAGTTTGTGAGCAAAATGATGCTTACGAGAAATCTGAGAGAAAGCAACAT 634
 QY 160 ArgArgGlyAsnMet----- 164

Db 635 GTTCGGGAGCAGAGTGTGGAGCAGGCTGCAACTTAATTGGCTATGACCTGACGCT 694
Qy 165 -----LeuH:sgly-----TyrPheaspGlnGluAlaIaGly 175
Db 635 GAAGTCAGCAGACCTCTTACGCGCGCATGGCTTCTTCATCCACTTGATGCTGCTGT 754
Qy 176 GluaspPro---GlnTyrGlyTyr-----GluaspGlnGluIaaspTyrGluSerAla 192
Db 755 GAACCCACCTTCATGATGGGTACCTGACAGCATCATGAG-----796
Qy 193 LeuAlaSerAsnGlnGlyAlaAsnAspLeuTyr 203
Db 797 ---GGATGAACAGTGCCTGATGAACACTTAC 826
RESULT 7
US-08-867-087B-16
; Sequence 16, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: At, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarkust Sparkman Campbell Leigh &
; ADDRESS: Winston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk, 3-1/2 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867, 087B
; FILING DATE: June 2, 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/323,449
; FILING DATE: October 14, 1994
; APPLICATION NUMBER: U.S. 08/485,981
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Alan, E.
; REGISTRATION NUMBER: 35,123
; REFERENCE/DOCKET NUMBER: 4630-47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1180 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; US-08-867-087B-16
Alignment Scores:
Pred. No.: 5.56e-26 Length: 1180
Score: 287.00 Matches: 76
Percent Similarity: 55.72% Conservative: 36
Best Local Similarity: 37.81% Mismatches: 65
Query Match: 23.60% Indels: 24
DB: 2 Gaps: 7
US-10-069-527-4 (1-232) x US-08-867-087B-16 (1-1180)
Qy 1 MetAlaargGlyLysIleGlnIleLysLeuIleGluAsnGlnThrAsnArgGlnValThr 20

Db 110 ATGGGAGAGGAGGAGGTGGAGCTGAAGAGATCGAAGAACAGATCAACAGGAGGTGAC 169
Qy 21 TyrSerLysArgArgAsnGlnIlePheLysLysAlaGlnGluLeuThrValLeuCyasp 40
Db 170 TTCGGCAACCGAGAGAAATGGGCTGCTCAAGAGGGGTGACAGCTCTCGGTCTGCGAC 229
Qy 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlyTyrIleSerPro 60
Db 230 GCGAGGTGCGCCCTATCATCTTCTCCAAACCGCGCAAGCTCTAGCATTTCTGACGCGC 289
Qy 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMet-----GlyTleasp 78
Db 290 CAAGCATGACCCAGAACTTTG---GAAAGATACCAAAATTCAGTTATGTGGGCGCAGAT 346
Qy 79 LeuTPrArgThrHisGluGlu-----SerMetLysAspThrLeuTyrLys 93
Db 347 ACTGCATTAACAGAACAGAAATAGTATGTCAGAACAGCCGCAATGAGTACTCTCAA 406
Qy 94 LeuLysGluIleAsnAsnLysLeuArgArgGlnIleArgGlnArgLeuGlyHisAspLeu 113
Db 407 CTGAAGCAGCGGCTGAAAATTTACAGAGACCCAAAGAACTTCTTGTGAGATCTT 466
Qy 114 AsnGlyLeuSerPheaspGluLeuLaserLeuAspAspGluMetGlnSerSerLeuasp 133
Db 467 GGGACACTTGCCATMAAAGAGCTAGAGCAGCTTGAGAAACACTTGATTCCTTGAGG 526
Qy 134 AlaIleArgGln---ArgLysTyrHisValIleLysThrGlnThrGlnThrThrLysLys 152
Db 527 CACATTAGATCCACAGAGACACAGCATATGCTTGATCAGCTCATGATCTCCAGAGAGG 586
Qy 153 LysVal-----LysAsnLeuGluGlnArgArgGly 162
Db 587 GAACAAATGTGTGTGAAGCAAAATAGCTCTCAGAAAGAAAACGTGAGAGAG-----AGC 640
Qy 163 AsnMetLeuHisGlyTyrPheaspGlnGluAlaIaGlyLysAspProGlnTyrGlyTyr 182
Db 641 AACCGTTGCATGAGCAAGCTGTGGAGACGCGCC-----ACCTACTGCGCTAC 691
Qy 183 Gln 183
Db 692 GAG 694
RESULT 8
US-09-611-659A-3
; Sequence 3, Application US/09611659A
; Patent No. 6514760
; GENERAL INFORMATION:
; APPLICANT: Mao, Long
; APPLICANT: Rod, Wang
; TITLE OF INVENTION: Jointless Gene of Tomato
; FILE REFERENCE: C218 1010
; CURRENT APPLICATION NUMBER: US/09/611,659A
; CURRENT FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; US-09-611-659A-3
Alignment Scores:
Pred. No.: 5.47e-26 Length: 798
Score: 285.00 Matches: 72
Percent Similarity: 53.74% Conservative: 50
Best Local Similarity: 31.72% Mismatches: 73
Query Match: 23.44% Indels: 32
DB: 4 Gaps: 6
US-10-069-527-4 (1-232) x US-09-611-659A-3 (1-798)
Qy 1 MetAlaargGlyLysIleGlnIleLysLeuIleGluAsnGlnThrAsnArgGlnValThr 20

```

Db      1  ATGGCTAGAGAAAAATTCAAGATCAAGAAATAGTAATCTCCACAGCAAGCAAGCTTACA 60
Qy      21  TysSerLysArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAsp 40
        61  TTTTCAAGAGAGAGAGAGCTTTATTCAGAGAAAGCTGAGAGAACTTCTGCTCTGAT 120
Qy      41  AlalysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
        121  GCTGATGTTGCTCTCATCATTTCTCTCTCTAGTGAATAATTATTTGACTATTCTAGCTCA 180
Qy      61  ThrThrThr-----ThylsSerMetTyrAspAspTyr 71
        181  AGCATGAAACAAATTCTTGAGAGGCGTGAATTTGCATTCGAAAAATCTGAAAAATTTGAT 240
Qy      72  GlnLysThrMetGlyIleAspLeuTyrArgThrHisGlnGluSerMetLysAspThrLeu 91
        241  CAACCATCACTGCACTTCACTTCAAGAAATAGCAACTACTCCAGATTAAAGC----- 294
Qy      92  TrpLysLeuLysGluIleAsnAsnLysLeuArgArgGluIleArgGlnArgLeuGlyHis 111
        295  -----AAGGAAATTTCCGAAAAAAGTCACTCA-----TTAAGCCAAATGAGGAGAGAA 342
Qy      112  AspLeuAsnGlyLeuSerPheAspGluLeuAlaSerLeuAspAspGluMetGlnSerSer 131
        343  GAACCTTCAAGAGACTAAATTTGAGAGATTGCAACAAATTGAGAGAGATCTCTGAAACTGGA 402
Qy      132  LeuAspAlaIleArgGlnArgLys-----139
        403  TTGAGCCGCGTCAATGAGAGAAAGGCTGATTAATAATATGAGAGAGATCAACCACTCCAA 462
Qy      140  -----TyrHisValIleLysThrGlnThrGlnThrLysLysValLysAsn 156
        463  CAAAAGGATGATCACTTAATGGA---GAAATGAAAAATTAAGCAACAGTGAATGAG 519
Qy      157  LeuGlnGlnArgArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaIleGlyGlu 176
        520  ATATCTAATAATAATAATAATAATAATAATGATATGAGAGAGAGAGAGATGATTAATTT 579
Qy      177  AspProGlnTyrGlyTyrGluAspAsnGluGly---AspTyrGluSerAlaLeuAlaLeu 195
        580  GAACCGAAGAAATGAGATTAAATAATAATAATAATGAAGATGCCCAATCATCTGAATCAGTA 639
Qy      196  SerAsnGlyAlaAsnAsnLeu 202
        640  ACAATCCATGTAATCACTCAATT 660
Db
RESULT 9
US-09-611-659A-2
; Sequence 2, Application US/09611659A
; Patent No. 6514760
; GENERAL INFORMATION:
; APPLICANT: Rod, Long
; APPLICANT: Mao, Long
; TITLE OF INVENTION: Jointless Gene of Tomato
; FILE REFERENCE: C218 1010
; CURRENT APPLICATION NUMBER: US/09/611,659A
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1010
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-611-659A-2

Alignment Scores:
Pred. No.: 7 79e-26 length: 1010
Score: 285.00 Matches: 72
Percent Similarity: 53.74% Conservative: 50
Best Local Similarity: 31.72% Mismatches: 53
Query Match: 23.44% Indels: 32
DB: 4 Gaps: 6

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US-10-069-527-4 (1-232) x US-09-611-659A-2 (1-1010)
Qy      1  MetAlaArgGlyLysIleGluIleLysLeuIleGluAsnGlnThrAsnArgGlnValThr 20
        79  ATGGCTAGAGAAAAATTCAAGATCAAGAAATAGTAATCTCCACAGCAAGCAAGCTTACA 138
Db
Qy      21  TysSerLysArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAsp 40
        139  TTTTCAAGAGAGAGAGCTTTATTCAGAGAAAGCTGAGAGAACTTCTGCTCTGAT 198
Db
Qy      41  AlalysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
        199  GCTGATGTTGCTCTCATCATTTCTCTCTCTAGTGAATAATTATTTGACTATTCTAGCTCA 258
Qy      61  ThrThrThr-----ThylsSerMetTyrAspAspTyr 71
        259  AGCATGAAACAAATTCTTGAGAGGCGTGAATTTGCATTCGAAAAATCTGAAAAATTTGAT 318
Db
Qy      72  GlnLysThrMetGlyIleAspLeuTyrArgThrHisGlnGluSerMetLysAspThrLeu 91
        319  CAACCATCACTGCACTTCACTTCAAGAAATAGCAACTACTCCAGATTAAAGC----- 372
Qy      92  TrpLysLeuLysGluIleAsnAsnLysLeuArgArgGluIleArgGlnArgLeuGlyHis 111
        373  -----AAGGAAATTTCCGAAAAAAGTCACTCA-----TTAAGCCAAATGAGGAGAGAA 420
Qy      112  AspLeuAsnGlyLeuSerPheAspGluLeuAlaSerLeuAspAspGluMetGlnSerSer 131
        421  GAACCTTCAAGAGACTAAATTTGAGAGATTGCAACAAATTGAGAGAGATCTCTGAAACTGGA 480
Db
Qy      132  LeuAspAlaIleArgGlnArgLys-----139
        481  TTGAGCCGCGTCAATGAGAGAAAGGCTGATTAATAATATGAGAGAGATCAACCACTCCAA 540
Qy      140  -----TyrHisValIleLysThrGlnThrGlnThrLysLysValLysAsn 156
        541  CAAAAGGATGATCACTTAATGGA---GAAATGAAAAATTAAGCAACAGTGAATGAG 597
Qy      157  LeuGlnGlnArgArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaIleGlyGlu 176
        598  ATATCTAATAATAATAATAATAATAATAATGATATGAGAGAGAGAGATGATTAATTT 657
Db
Qy      177  AspProGlnTyrGlyTyrGluAspAsnGluGly---AspTyrGluSerAlaLeuAlaLeu 195
        658  GAACCGAAGAAATGAGATTAAATAATAATAATAATGAAGATGCCCAATCATCTGAATCAGTA 717
Qy      196  SerAsnGlyAlaAsnAsnLeu 202
        718  ACAATCCATGTAATCACTCAATT 738
Db
RESULT 10
US-08-867-087B-12
; Sequence 12, Application US/08867087B
; Patent No. 5990386
; GENERAL INFORMATION:
; APPLICANT: An, Gynheung
; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh &
; ADDRESS: Winston, LLP
; STREET: One World Trade Center
; STREET: 121 S.W. Salmon Street
; STREET: Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: United States of America
; ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible

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/ OPERATING SYSTEM: MS DOS
/ SOFTWARE: WordPerfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/067,0878
/ FILING DATE: June 2, 1997
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: U.S. 08/323,449
/ FILING DATE: October 14, 1994
/ APPLICATION NUMBER: U.S. 08/485,981
/ FILING DATE: June 7, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dow, Alan. E.
/ REGISTRATION NUMBER: 35,123
/ REFERENCE/DOCKET NUMBER: 4630-47071
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (503) 226-7391
/ TELEFAX: (503) 228-9446
/ INFORMATION FOR SEQ ID NO. 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1043 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double stranded
/ TOPOLOGY: linear
/
/ US-08-867-087B-12
/
/ Alignment Scores:
/ Pred. No.: 2.57e-25 Length: 1043
/ Score: 281.00 Matches: 75
/ Percent Similarity: 50.48% Conservative: 30
/ Best Local Similarity: 36.06% Mismatches: 83
/ Query Match: 23.11% Indels: 20
/ DB: Gaps: 6
/
/ US-10-069-527-4 (1-232) x US-08-867-087B-12 (1-1043)
/
/ QY 1 MetAlaArgGlyLysIleGluIleLysLeuIleGlnLysGlnThrAsnArgGlnValThr 20
/ DB 34 ATGGGAGGCGGAGAAAGTTGAGCTGACGACGCTGACAGAACAGATCAACAGCGCTGAC 93
/ QY 21 TySerIysArgArgGlnGlyIlePheLysLysLacIleGlnLysLeuThrValLeuCyasp 40
/ DB 94 TTCGCCAAGCGCCGCAACGCGCTCTCCAGAGGCGCTACAGAGCTGCTGCTCTGCGGAC 153
/ QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluIleSerPro 60
/ DB 154 GCCAGGCTGGCGCTCATCTATCTTCTCCAGCGCGGCGGCAAGCTTACGAGTTCGCGACGCC 213
/ QY 61 ---ThrThrThrThrLysSerMetTyr-----AspAspTyr 71
/ DB 214 GGCATACCAAGACTTTAGAAAGTACCAATGTTGCTACAAATGCTCAAGATTCAC 273
/ QY 72 GlnLysThrMetGlyIleAspLeuThrArgThrHisGlnLysSerMetLysAspThrLeu 91
/ DB 274 AATGCATCTTCTGAAATCTCAGAGCTGG---TACCATGAAATGCA----- 315
/ QY 92 TrpLysLeuLysGlnIleAsnAsnLysLeuArgArgGlnIleArgGlnArgLeuGlnHis 111
/ DB 316 ---AAGTTGAAGCAAAATTGAAGCTTTTCACGCGCACTCAAGGCACTTCTGGGGAG 372
/ QY 112 AspLeuAsnGlyLeuSerPheAspGlnLeuAlaSerLeuAspAspGlnMetGlnSerSer 131
/ DB 373 GATCTTGACACCTCAGACCGTCAAGAAATTCACAGCTGAGAAACAGCTTGAAATGCA 432
/ QY 132 LeuAspAlaIleArgGlnArgLysTyrHisValIleLysThrGlnThrArgThrLys 151
/ DB 433 CTATCAAGCGCGAGACAGAGAAAGACCACTATATGACACAGGTGAGGAACTTCC 492
/ QY 152 LysLysValLysAsnLeuGlnArgArgGlyAsnMetLeuHisGlyTyrPheAspGln 171
/ DB 493 AGAAGGAGCGTACGCTGGGTGAATTAATAGCAACTCAAGAC-----AAGCTC 543
/ QY 172 GluAlaIleGlnAspProGlnTyrGlyTyrGlnAspAsnGlnLysAspTyrGlnSer 191

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/ DB 544 GAGCTGAAGCTTCCACGACACTAC---AAGGCATGACAGACCTCTGAGCTAG 600
/ QY 192 AlaLeuAlaLeuSerAsnGlnVala 199
/ DB 601 GCGCGCGTGTGAGAAATGCGCC 624

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RESULT 11

US-09-067-800-1

Sequence 1, Application US/09067800

Patent No. 6198024

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.

TITLE OF INVENTION: Ferrandiz, Cristina

TITLE OF INVENTION: Seed Plants Characterized by Delayed

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESS: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/09/067,800

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 2948

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO. 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1062 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 101..827

NAME/KEY: misc_feature

LOCATION: 1062

OTHER INFORMATION: /note= "There is a poly(A) tail at

OTHER INFORMATION: the end."

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..1062

OTHER INFORMATION: /note= "Nucleotide and Deduced

OTHER INFORMATION: Amino Acid Sequences of the AGUs cDNA clone."

US-09-067-800-1

Alignment Scores:

Pred. No.: 3.51e-25 Length: 1062

Score: 280.00 Matches: 72

Percent Similarity: 50.42% Conservative: 48

Best Local Similarity: 30.25% Mismatches: 80

Query Match: 23.03% Indels: 38

DB: Gaps: 7

US-10-069-527-4 (1-232) x US-09-067-800-1 (1-1062)

QY 1 MetAlaArgGlyLysIleGluIleLysLeuIleGlnLysGlnThrAsnArgGlnValThr 20

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Db      101 ATGGGAGAGAGTGGTTCAGCTGAGAGATAGAGCAACCAATGACCAAGTTACT 160
Qy      21 Tyrserysargarsanglylephelyslysalnglnuleuthrvalleucysasp 40
      161 TTCTCAAGAGAGAGTGGTTCAGCTGAGAGATAGAGCAACCAATGACCAAGTTACT 220
Qy      41 Alalysvalserleullemetleuseranthrashnlymethisglutrylleserpro 60
      221 GCTGAGGTGCTCTCATGCTCTTCTTCCAAAGCAACCTTCGAATATTCACCGAC 280
Qy      61 Thrthrthrthrlyssermet-----tyraspasytyr-----glnlysthr 74
      281 TCTTGACATGAGAGATCTTGAAAGCTATATGCTATATATATTCAGACCAACACTT 340
Qy      75 Metglylleaspleutrpargthrhisglulusermetlysaspthrleutrplysleu 94
      341 GTTGCCGAGAGCGTTCCAAAGTGAAT-----TGGGTCTA 379
Qy      95 Lysglulleasnleuasnlyleuargglulle-----Arglnhargleu 109
      380 GAACATGCTTAAGCTCAAGGCAAGAGTTGAGTCTTGAGAAACAACCAAAAGATTATG 439
Qy      110 GlyhisaspleuasnglyleuserpheaspglyleuAlaserleuaspgluwetgln 129
      440 GGGGAAGATCTTGATTCGTTGAGCTTGAGAGAGCTCCAAAGCTTGAGACATCAGTCAT 499
Qy      130 SerSerleuaspaAlallearglnarglysthrhisvalleylesthrthrglnthr 149
      500 GCAGCTATCAAGAGATTAGGTCAAGAAACCAAGCTATGTTGCAATTCATCTGCG 559
Qy      150 ThrlysllysvallyleasnleuuglnargarggluysanmetleuHisglityrphe 169
      560 CTCGAGAGAGAGATTAAGCTTGCAAGATCAACAATTCGCTTCTCAAAAAGATTAG 619
Qy      170 Aspginglu---Alalaglygluasp-----Arglnhargleu 177
      620 GAGAGGAGAGAGAAACGGGTGACGAGAGAGCAATTAGTCCATGCTCCAACTTCT 679
Qy      178 -----ProglntyrlytyrgluaspaangluylaspytyrgluserAlaleu 193
      680 TCAAGTCTTCTGCTCAATATCTGCGTAACCTCTCCAGAGATGCGTTGTGAGAGAGT 739
Qy      194 AlaleuserasnglyAlaasnleuutythrphesleuHisleuproasn 211
      740 GGGGAGAGAGACGGTGTGATCGTCTGAGC-----GAACCAAC 781
Db
RESULT 12
US-09-105-652-1
; Sequence 1, Application US/09105652
; Patent No. 6239068
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Martienssen, Robert
; APPLICANT: Ferrandiz, Cristina
; APPLICANT: Gu, Qing
; TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant
; FILE REFERENCE: P-UD 3040
; CURRENT APPLICATION NUMBER: US/09/105,652
; EARLIER FILING DATE: 1998-06-26
; EARLIER FILING DATE: 1997-06-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(826)
; FEATURE:
; NAME/KEY: polyA_signal

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; LOCATION: (1061)
US-09-105-652-1
Alignment Scores:
Pred. No.: 3,51e-25 Length: 1062
Score: 280.00 Matches: 72
Percent Similarity: 50.42% Conservative: 48
Best Local Similarity: 30.25% Mismatches: 80
Query Match: 23.03% Indels: 38
DB: 3 Gaps: 7
US-10-069-527-4 (1-232) x US-09-105-652-1 (1-1062)
Qy      1 MetAlaArgGlylysleuglyleuAlleuglnthrasnarglnvalthr 20
      101 ATGGGAGAGAGTGGTTCAGCTGAGAGATAGAGCAACCAATGACCAAGTTACT 160
Qy      21 Tyrserysargarsanglylephelyslysalnglnuleuthrvalleucysasp 40
      161 TTCTCAAGAGAGAGTGGTTCAGCTGAGAGATAGAGCAACCAATGACCAAGTTACT 220
Qy      41 Alalysvalserleullemetleuseranthrashnlymethisglutrylleserpro 60
      221 GCTGAGGTGCTCTCATGCTCTTCTTCCAAAGCAACCTTCGAATATTCACCGAC 280
Qy      61 Thrthrthrthrlyssermet-----tyraspasytyr-----glnlysthr 74
      281 TCTTGACATGAGAGATCTTGAAAGCTATATGCTATATATATTCAGACCAACACTT 340
Qy      75 Metglylleaspleutrpargthrhisglulusermetlysaspthrleutrplysleu 94
      341 GTTGCCGAGAGCGTTCCAAAGTGAAT-----TGGGTCTA 379
Qy      95 Lysglulleasnleuasnlyleuargglulle-----Arglnhargleu 109
      380 GAACATGCTTAAGCTCAAGGCAAGAGTTGAGTCTTGAGAAACAACCAAAAGATTATG 439
Qy      110 GlyhisaspleuasnglyleuserpheaspglyleuAlaserleuaspgluwetgln 129
      440 GGGGAAGATCTTGATTCGTTGAGCTTGAGAGAGCTCCAAAGCTTGAGACATCAGTCAT 499
Qy      130 SerSerleuaspaAlallearglnarglysthrhisvalleylesthrthrglnthr 149
      500 GCAGCTATCAAGAGATTAGGTCAAGAAACCAAGCTATGTTGCAATTCATCTGCG 559
Qy      150 ThrlysllysvallyleasnleuuglnargarggluysanmetleuHisglityrphe 169
      560 CTCGAGAGAGAGATTAAGCTTGCAAGATCAACAATTCGCTTCTCAAAAAGATTAG 619
Qy      170 Aspginglu---Alalaglygluasp-----Arglnhargleu 177
      620 GAGAGGAGAGAGAAACGGGTGACGAGAGAGCAATTAGTCCATGCTCCAACTTCT 679
Qy      178 -----ProglntyrlytyrgluaspaangluylaspytyrgluserAlaleu 193
      680 TCAAGTCTTCTGCTCAATATCTGCGTAACCTCTCCAGAGATGCGTTGTGAGAGAGT 739
Qy      194 AlaleuserasnglyAlaasnleuutythrphesleuHisleuproasn 211
      740 GGGGAGAGAGACGGTGTGATCGTCTGAGC-----GAACCAAC 781
Db
RESULT 13
US-09-349-677-1
; Sequence 1, Application US/09349677
; Patent No. 6288305
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Ferrandiz, Cristina
; TITLE OF INVENTION: Seed Plants Characterized by Delayed
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP

```

```

/ STREET: 4370 La Jolla Village Drive, Suite 700
/ CITY: San Diego
/ STATE: California
/ COUNTRY: United States
/ ZIP: 92122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/349,677
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/067,800
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-UD 2948
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1062 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 101..827
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1062
/ OTHER INFORMATION: /note= "There is a poly(A) tail at
/ OTHER INFORMATION: the end."
/ NAME/KEY: misc_feature
/ LOCATION: 1..1062
/ OTHER INFORMATION: /note= "Nucleotide and Deduced
/ OTHER INFORMATION: Amino Acid Sequences of the ACH8 cDNA clone."
US-09-349-677-1

Alignment Scores:
Pred. No.: 3,51e-25 Length: 1062
Score: 280.00 Matches: 72
Percent Similarity: 50.42% Conservative: 48
Best Local Similarity: 30.25% Mismatches: 80
Query Match: 23.03% Indels: 38
DB: 3 Gaps: 7

US-10-069-527-4 (1-232) x US-09-349-677-1 (1-1062)
QY 1 MetAlaArgGlyLysIleGluIleLysLeuIleGluAsnGlnThrAsnArgGlnValThr 20
DB 101 ATGGAGAGAGTGGTTCAGCTGAGAGATGAGACAAAGTCAATGCGCAAGTACT 160
QY 21 TyrSerLysArgArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAsp 40
DB 161 TTCTCAAGAGAGAGGTGTGGTTGGCTCAAGAAAGCTCAGTCTCTGTTCTTCGCAAT 220
QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
DB 221 GCTGAGGTTCTCTCATCGTCTCTCTTCCAAAGGCAACTCTGCAATATTCACCGAC 280
QY 61 ThrThrThrThrLysSerMet-----TyrAspAspTyr-----GlnLysThr 74
DB 281 TCTTGATGAGAGGATCTTGAACGCTATGATGCTATTATTAATTCAGACAAACAACTT 340
QY 75 MetGlyLysLeuPheLeuTyrArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeu 94

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DB 341 GTTGGCCGAGACGTTTCACAAAGTGAAAT-----TGGGTTCA 379
QY 95 LysGluIleAsnAsnLysLeuArgGluIle-----ArgGlnArgLeu 109
DB 380 GAACATGCTTAAGCTCAAGGCAAGAGTGGTACTTGAAGAACAAAGAAATTTATG 439
QY 110 GlyHisAspLeuAsnGlyLeuSerPheAspGluLeuAlaSerLeuAspGluMetGln 129
DB 440 GGGAGAGATCTTGATTCGTTGAGCTTGAAGAGCTCCAAAGCTTGAGACATCAGCTCAT 499
QY 130 SerSerLeuAspAlaIleArgGlnArgLysTyrHisValIleLysThrGlnThrGlnThr 149
DB 500 GGAGCTATCAAGCATTTAGTCAAGAAACCAAGCTATGTCGATTCATCTCGC 559
QY 150 ThrLysLysValLysAsnLeuGlnIleArgGluArgGluAsnMetLeuHisGlyTyrPhe 169
DB 560 CTCGACAGAGAGATTAAGCTTGCAGAGATCACAAACATTCGCTTCTCAAAAAGATTAG 619
QY 170 AspGlnGlyLysAlaGlyLysAsp----- 177
DB 620 GAGAGGAGAGAGAAACGGGTGACAGAGACAAATTAGTCAATGCTCCAACTCTTCT 679
QY 178 -----ProGlnTyrGlyTyrGluAspAsnGluGlyAspTyrGluSerAlaLeu 193
DB 680 TCAATCTTTCGCTCAATTAAGCTTAACCTCTCCAGATGCTTGTGAGAGAGCTT 739
QY 194 AlaLeuSerAsnGlyAlaAsnAsnLeuTyrThrPheHisLeuHisProAsn 211
DB 740 GGGGAGAGAGAGAGGTGTCATGCTGCTGAGG-----GAACCAAC 781

RESULT 14
US-09-708-584-1
/ Sequence 1, Application US/09708584
/ Patent No. 6541683
/ GENERAL INFORMATION:
/ APPLICANT: Vancovsky, Martin F.
/ APPLICANT: Marienssen, Robert
/ APPLICANT: Ferrandiz, Cristina
/ APPLICANT: Gu, Qing
/ TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant
/ FILE REFERENCE: P-UD 3040
/ CURRENT APPLICATION NUMBER: US/09/708,584
/ PRIOR FILING DATE: 2000-11-07
/ PRIOR APPLICATION NUMBER: 09/105,652
/ PRIOR FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: 60/051,030
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 1062
/ TYPE: DNA
/ ORGANISM: Arabidopsis sp.
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (101)..(826)
/ NAME/KEY: polyA signal
/ LOCATION: (1061)
US-09-708-584-1

Alignment Scores:
Pred. No.: 3,51e-25 Length: 1062
Score: 280.00 Matches: 72
Percent Similarity: 50.42% Conservative: 48
Best Local Similarity: 30.25% Mismatches: 80
Query Match: 23.03% Indels: 38
DB: 4 Gaps: 7

US-10-069-527-4 (1-232) x US-09-708-584-1 (1-1062)
QY 1 MetAlaArgGlyLysIleGluIleLysLeuIleGluAsnGlnThrAsnArgGlnValThr 20

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Db 101 ATGGAGAGAGTACGGTTCAGCTGAGAGATAGAGAACAGATCAATAGGCAAGTTACT 160
Qy 21 Tysrlysaarsaarsnglyilephelysvalaglnuleuthrvalleyuasp 40
Db 161 TTCCTAAAGAGAGAGTGGTGGTTCCTCAAGAGAGCTCAAGATCTCTGTTCTGGCAT 220
Qy 41 Alalyvalserleulemetleuseranthrasnlysmethisglutrylleserpro 60
Db 221 GCTGAGGTGGCTCTCATGCTCTCTCTTCCAAAGGCAAACTCTCGAATATTCACACGAC 280
Qy 61 Thrtthrtthrtlysermet-----Tyrasaptryr-----Glnlyethr 74
Db 281 TCTTGACGAGAGAGATCTTGACGCTATGATCGCTATTTATATTCAGACAAACACTT 340
Qy 75 Metgylileaspleletrparthrtthrtthrtthrtthrtthrtthrtthrtthrt 94
Db 341 GTTGCCGAGAGAGCTTCAAGAGTAAAT-----TGGGTCTA 379
Qy 95 Lysglulileasnlyleuargarglule-----Arglnargleu 109
Db 380 GAACATGCTTAAGCTCAAGCAAGAGTGAAGTGAAGAAACAAAGAAATTTATG 439
Qy 110 Glyhisaspleuasnglyleuserpheaspguleualaserleuaspsglumecgin 129
Db 440 GGGGAAGATCTTGATTCGTTGAGCTTGAAAGAGCTCCAAAGCTTGAGACATCAGTCGAT 499
Qy 130 SerSerleuaspsalilearglnarglystyrhisvalilelyethrthrtthrtthrt 149
Db 500 GCAAGCTATCAAGAGATGATGCAAGAAAGCAAGATGATGCAAGTCAATCTGCG 559
Qy 150 Thrlysllylevallyleasnleuuglnargarglyuanmetleuhsiglytyrph 169
Db 560 CTCGAAAGAGAGATTAAGCTTCGCAAGATCAACAAATTCGCTTCAAAAGATTAAG 619
Qy 170 Aspginglu---Alalaglygluasr-----177
Db 620 GAG 679
Qy 178 -----Prglnlyrlytyrlyleuasnglyleuasprtyrlyserleu 193
Db 680 TCAAGTCTTCTGCTCAATCAATGCGTAACCTCTCCAGAGAGAGAGAGAGAGAGAG 739
Qy 194 Alalyvalserleulemetleuseranthrasnlysmethisglutrylleserpro 211
Db 740 GGGGAG 781

RESULT 15
US-09-067-800-7
Sequence 7, Application US/09067800
Patent No. 6198024
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Characterized by Delayed
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,800
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2948
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 959 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 78..818
NAME/KEY: misc feature
LOCATION: 1..959
OTHER INFORMATION: /note= "AGUS cDNA and deduced
OTHER INFORMATION: protein sequences."
US-09-067-800-7

Alignment Scores:
Pred. No.: 4,01e-25 Length: 959
Score: 279.00 Matches: 74
Percent Similarity: 47.11% Conservative: 40
Best Local Similarity: 30.58% Mismatches: 72
Query Match: 22.94% Gaps: 56
Indels: 6

US-10-069-527-4 (1-232) x US-09-067-800-7 (1-959)
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Qy 41 Alalyvalserleulemetleuseranthrasnlysmethisglutrylleserpro 57
Db 243 GCTGAGGTGCTCTGTCATCTCTCCACTCGAGCGCTCTTACAGAGTACGCCAACAC 302
Qy 58 -----IleSerProThr 61
Db 303 AGTGTGAG 362
Qy 62 ThrtthrtthrtlysermettyrasaptryrGlnlyethrmetGlyleaspleutparg 81
Db 363 ACCATCAACGAGAGATTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 404
Qy 82 ThrtthrtthrtlysermettyrasaptryrGlnlyethrmetGlyleaspleutparg 101
Db 405 -----TCAAACTC 413
Qy 102 Argarglule-----ArgGlnargleuGlnhisaspleuasn 114
Db 414 CGGAGAGAGAGTGGGAGCATTCAGAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 473
Qy 115 GlyleuserpheaspguleualaserleuaspsglumecGlnserSerleuaspsala 134
Db 474 TCTTGAACTTTAAG 533
Qy 135 Ilearglnarglytyrhisvalilelyethrthrtthrtthrtthrtthrtthrtthrt 154
Db 534 GTCGATCCAG 587
Qy 155 LysasnleuuglnargarglyasmetleuhsiglytyrphaspgingluAlaAla 174
Db 588 AGGGAATCGAGTGCAGAAAGATTAAGTATCTCCGCTCAAGATTAAGTAAAGAGAGAG 647

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QY 175 GlyIuaaspProGlnTyrglyTyrgIuaaspangIuIasp---TyrgIuaSerAlaIeu 193
Db 648 GGTCTACAGCAACAAGATCGATGTGATACATCAAGGACAGTTACAGAGTCGGGTGT 707
QY 194 AlaIeuSerAsnGlyAla-----AsnAsnLeuTyrrhrPheHisIeuHis 209
Db 708 ACTTCTCTCACCAAGTCGGGGCAGTATACCGAATTATATTGCGGTTACCTTCTTGA 767
QY 210 ProAsn 211
Db 768 CCGAAT 773

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Search completed: September 26, 2004, 11:14:11
 Job time : 76.1432 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2004, 07:03:56; Search time 473.861 Seconds
(without alignments)
2479.773 Million cell updates/sec

Title: US-10-069-527-4
Perfect score: 1216
Sequence: 1 MARKERIKLEIENQTNQVT.....HHGSSISGSIITHLIDRLA 232

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
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Searched: 3337386 seqs, 2532474682 residues

Total number of hits satisfying chosen parameters: 6674772

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database: Published Applications_NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No. Score Match Length DB ID Description

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709.5	58.3	681	15	US-10-104-580-3	Sequence 3, Appl1	709.5	58.3	681	15	US-10-104-580-2	Sequence 2, Appl1	655.5	53.9	1050	13	US-10-425-114-12758	Sequence 12758, A	652	53.6	1231	13	US-10-425-114-15025	Sequence 15025, A	640.5	52.7	1232	13	US-10-425-114-11957	Sequence 11957, A	631.5	51.9	1155	13	US-10-424-559-66649	Sequence 66649, A	612	50.3	644	17	US-10-021-323-8631	Sequence 8631, Ap	604.5	49.7	1036	13	US-10-424-559-120794	Sequence 120794, A	576.5	47.4	871	13	US-10-425-114-10670	Sequence 10670, A	553.5	45.5	681	16	US-10-260-238-5530	Sequence 5530, Ap	533	43.0	488	12	US-09-732-627A-4479	Sequence 4479, Ap	474	39.0	2237	13	US-10-425-114-11190	Sequence 11190, A	471	38.7	2718	13	US-10-424-559-130795	Sequence 130795, A	454	37.3	407	12	US-09-922-293-3294	Sequence 3294, A	435	35.8	425	12	US-09-922-293-14	Sequence 14, Appl	419.5	34.5	4285	15	US-10-104-580-1	Sequence 1, Appl1	410	33.7	401	12	US-09-922-293-15	Sequence 15, Appl	410	33.7	432	12	US-09-922-293-16	Sequence 16, Appl	410	33.7	432	12	US-10-437-963-29598	Sequence 29598, A	398	32.7	928	17	US-10-437-963-29598	Sequence 32958, A	396.5	32.6	951	12	US-09-922-293-3447	Sequence 3447, Ap	391	32.2	951	17	US-10-767-793-12121	Sequence 12121, Ap	386	31.7	360	12	US-09-922-293-15	Sequence 15, Appl	385	31.6	639	17	US-10-021-323-8682	Sequence 8682, Ap	383	31.5	1007	13	US-10-425-114-14870	Sequence 14870, A	380.5	31.3	1021	13	US-10-424-559-65326	Sequence 65326, A	379.5	31.2	601	17	US-10-021-323-13542	Sequence 13542, A	375	30.8	649	17	US-09-922-293-3446	Sequence 3446, Ap	370	30.4	474	12	US-09-732-627A-4667	Sequence 4667, Ap	368.5	30.3	900	13	US-10-425-114-10295	Sequence 10295, A	368.5	30.3	932	13	US-09-732-627A-3282	Sequence 3282, Ap	365	28.9	535	12	US-09-732-627A-337	Sequence 337, App	349	28.7	309	12	US-09-732-627A-380	Sequence 380, App	347	28.5	340	12	US-09-922-293-3293	Sequence 3293, Ap	332	27.3	298	12	US-09-922-293-3293	Sequence 3293, Ap	332	27.3	298	12	US-10-278-536-238	Sequence 536, App	331.5	27.3	896	15	US-10-412-699B-55	Sequence 699, Ap	331.5	27.3	896	15	US-09-922-293-3282	Sequence 3282, Ap	327	26.9	285	12	US-10-094-458A-7	Sequence 7, Appl1	326	26.8	10140	15	US-09-922-293-3442	Sequence 3442, Ap	315	25.9	253	12	US-10-260-238-3321	Sequence 3321, Ap	315	25.9	1185	16	US-10-437-963-9922	Sequence 9922, Ap	313	25.7	3265	17	US-10-260-238-1150	Sequence 1150, Ap	310.5	25.5	933	16	US-10-260-238-5927	Sequence 5927, Ap	310.5	25.5	783	17	US-10-437-963-10714	Sequence 10714, A

ALIGNMENTS

RESULT 1
US-10-104-580-3
; Sequence 3, Application US/10104580
; Publication No. US20030035628A1
; GENERAL INFORMATION:
; APPLICANT: Strauss et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; TITLE OF INVENTION: Poplar and other plant species.
; FILE REFERENCE: 62486
; CURRENT APPLICATION NUMBER: US/10/104,580
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 09/410,464
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/287,700
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,851
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa

FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(681)
US-10-104-580-3

Alignment Scores:

Pred. No.: 3,78e-75 Length: 681
Score: 709.50 Matches: 149
Percent Similarity: 72.38% Conservative: 24
Best Local Similarity: 62.34% Mismatches: 45
Query Match: 58.35% Indels: 21
DB: 15 Gaps: 5

US-10-069-527-4 (1-232) x US-10-104-580-3 (1-681)

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QY      1 MetAlaArgGlyLysIleGluIleLeuIleGluLeuGlnThrAsnArgGlnValThr 20
DB      1 ATGGGTCGCGGAAAGATTGAATCAAGAGATCGAAAACCCCAAGACGCAAGTCACC 60

QY      21 TySerLysArgArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCyasp 40
DB      61 TACTGAGAGAGAGAAATGATATTTCAGAGAAAGCCCAAGACTCAGTACTTGTGAT 120

QY      41 AlaLysValSerIleuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
DB      121 GCTAAGGTCCTCTTATCATGTCTCTCCAACTAACAACCAATGAGTACATTAGCCCC 180

QY      61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTyr 80
DB      181 TCACATCGACAAAGAGATCTACGATCAATATCAAGAACGTTTAGCATAGATCTGTGG 240

QY      81 ArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnAsnLys 100
DB      241 GGCACTCAATACGAGAAATGCAAGACAGACACTTGAGAGATGATATCAATCATATAG 300

QY      101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
DB      301 CTGAGACAAAGAAATCAGGACAGAGAGAGAGAGGCGCTGATGATCTGAGCATTTGATCAT 360

QY      121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
DB      361 CTGGCGCGCTTTGAGCAACATATGATCGAAGCCTTGATGTGTGGTGGCAGAGAGTAC 420

QY      141 HisValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeuGlnArg 160
DB      421 CATGTGATCAAAACAAACGAAACCTACAGAGAGAGAGTGAAGATTAGAGAGAGAGA 480

QY      161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaIleGlyLysAspProGlnTyr 180
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QY      181 GlyTyrGluAspAsnGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
DB      532 GGTTTAGTGACAAT-----GAGGCTGCTGTGCACTTCAAAATGGGCGCTCC 579

QY      201 AsnLeuTyrThrPheHisLeuHis-----ProAsnLeu 212
DB      580 AACCTCATCATTTCCGCTGATCAAGGCGACACACACACCATCTCCCTAATCTT 639

QY      213 HisHisGlyLysSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLeu 231
DB      640 CACCTT---GGAGATGATTGGAGCC-----CATGAACCTGCGCTT 678

RESULT 2
US-10-104-580-2
; Sequence 2, Application US/10104580
; Publication No. US20030033628A1
; GENERAL INFORMATION:
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 62486
; CURRENT APPLICATION NUMBER: US/10/104,580

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CURRENT FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: 09/410,464
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 09/287,700
PRIOR FILING DATE: 1999-04-06
PRIOR APPLICATION NUMBER: 60/080,851
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 946
TYPE: DNA
ORGANISM: Populus balsamifera subsp. trichocarpa

FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(684)
US-10-104-580-2

Alignment Scores:

Pred. No.: 6.13e-75 Length: 946
Score: 709.50 Matches: 149
Percent Similarity: 72.38% Conservative: 24
Best Local Similarity: 62.34% Mismatches: 45
Query Match: 58.35% Indels: 21
DB: 15 Gaps: 5

US-10-069-527-4 (1-232) x US-10-104-580-2 (1-946)

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QY      1 MetAlaArgGlyLysIleGluIleLeuIleGluLeuGlnThrAsnArgGlnValThr 20
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QY      21 TySerLysArgArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCyasp 40
DB      61 TACTGAGAGAGAGAAATGATATTTCAGAGAAAGCCCAAGACTCAGTACTTGTGAT 120

QY      41 AlaLysValSerIleuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
DB      121 GCTAAGGTCCTCTTATCATGTCTCTCCAACTAACAACCAATGAGTACATTAGCCCC 180

QY      61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTyr 80
DB      181 TCACATCGACAAAGAGATCTACGATCAATATCAAGAACGTTTAGCATAGATCTGTGG 240

QY      81 ArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnAsnLys 100
DB      241 GGCACTCAATACGAGAAATGCAAGACAGACACTTGAGAGATGATATCAATCATATAG 300

QY      101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
DB      301 CTGAGACAAAGAAATCAGGACAGAGAGAGAGGCGCTGATGATCTGAGCATTTGATCAT 360

QY      121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
DB      361 CTGGCGCGCTTTGAGCAACATATGATCGAAGCCTTGATGTGTGGTGGCAGAGAGTAC 420

QY      141 HisValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeuGlnArg 160
DB      421 CATGTGATCAAAACAAACGAAACCTACAGAGAGAGAGTGAAGATTAGAGAGAGAGA 480

QY      161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaIleGlyLysAspProGlnTyr 180
DB      481 CATGAAACCTCTTGATGAGATAT-----GAGGCAAAACTAGACATGACAGCTAT 531

QY      181 GlyTyrGluAspAsnGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
DB      532 GGTTTAGTGACAAT-----GAGGCTGCTGTGCACTTCAAAATGGGCGCTCC 579

QY      201 AsnLeuTyrThrPheHisLeuHis-----ProAsnLeu 212
DB      580 AACCTCATCATTTCCGCTGATCAAGGCGACACACACACCATCTCCCTAATCTT 639

QY      213 HisHisGlyLysSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLeu 231

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Db      640 CACCTT---GGAGATGATTTGGAGCC-----CATGAACCTTGGCCTT 678
RESULT 3
US-10-425-114-12758
/ Sequence 12758, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/   APPLICANT: Liu, Jingdong
/   APPLICANT: Zhou, Yihua
/   APPLICANT: Kovalic, David K.
/   APPLICANT: Screen, Steven E
/   APPLICANT: Tabaska, Jack E
/   APPLICANT: Cao, Yongwei
/   TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/   TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/   FILE REFERENCE: 38-21(5313)B
/   CURRENT APPLICATION NUMBER: US/10/425,114
/   CURRENT FILING DATE: 2003-04-26
/   NUMBER OF SEQ ID NOS: 73126
/   SEQ ID NO 12758
/   LENGTH: 1050
/   TYPE: DNA
/   ORGANISM: Glycine max
/   FEATURE:
/   OTHER INFORMATION: Clone ID: 701209467_FLI
US-10-425-114-12758

Alignment Scores:
Pred. No.:      2,11e-68      Length:      1050
Score:          655.50        Matches:      142
Percent Similarity: 72.50%    Conservative: 32
Best Local Similarity: 59.17% Mismatches:      51
Query Match:    53.91%        Indels:       15
DB:             13           Gaps:         7

US-10-069-527-4 (1-232) x US-10-425-114-12758 (1-1050)

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QY      21 TyrSerLysArgArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAsp 40
Db      118 TACTCCAGGCAAGCAAGATTCAGTAAAGTTGATGGAAAGCCCAAGCAAGTCACT 177
QY      41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
Db      178 GCCAAGGTTTCACCTATCATGTTCTTAAACCAACAGATGATGATTAATGACCT 237
QY      61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGly---IleAspLeu 79
Db      238 GGCCCTCAGCAAAAAGATCATGATCATGATCAGAAAGACTTGGGGATTTGATCTG 297
QY      80 TTPAArgThrHisGluGlnSerMetLysAspThrLeuTTPlyLysLeuLysGluIleAsn 99
Db      298 TGGCGTTCTCAGTATGAGAAATGCTTGAAACCTTGAAAGAGCTATGATTTAAACAC 357
QY      100 LysLeuArgArgGluIleArgGlnArgLeuGlyHis-----AspLeuAsnGlyLeuSer 117
Db      358 AAGCTCAGAGACAGATTCAGGATGATGATGATGATGATGATGATGATGATGATGATG 417
QY      118 PheAspGluLeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGln 137
Db      418 TTCACGCAACTCGCACTCTTGAAAGAGATTGGTTTCTTCATAGGGGAAAATACGAAA 477
QY      138 ArgLysTyrHisValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeu 157
Db      478 CGAAGTTCCACTGATTCACAAACAGCATGATCCTGACAGAAAAGTTTAAAGCCG 537
QY      158 GluGlnArgArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaIleGlyLys 177
Db      538 GAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 588

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QY      178 ProGlnTyrGlyTyrGluAspAsnGluGlyAspTyrGlnSerAlaLeuAlaSerAsn 197
Db      589 CCACAAATTTATTTTGGACAT---GAAAGAGACAGAGATTCAGCATTCAGTCACTGGCCAC 645
QY      198 GlyAlaAsnAsnLeuTyrThrPhe---HisLeuHisHisProAsnLeu----- 212
Db      646 GGGCCTCCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 705
QY      213 HisHisGlyGlySerSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLeuAla 232
Db      706 CACCAT-----TCTCAGGAGAGAAACCTTTAAACTGATGATCCTTGGCTTGGCT 756

RESULT 4
US-10-425-114-15025
/ Sequence 15025, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/   APPLICANT: Liu, Jingdong
/   APPLICANT: Zhou, Yihua
/   APPLICANT: Kovalic, David K.
/   APPLICANT: Screen, Steven E
/   APPLICANT: Tabaska, Jack E
/   APPLICANT: Cao, Yongwei
/   TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/   TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/   FILE REFERENCE: 38-21(5313)B
/   CURRENT APPLICATION NUMBER: US/10/425,114
/   CURRENT FILING DATE: 2003-04-26
/   NUMBER OF SEQ ID NOS: 73126
/   SEQ ID NO 15025
/   LENGTH: 1231
/   TYPE: DNA
/   ORGANISM: Glycine max
/   FEATURE:
/   OTHER INFORMATION: Clone ID: LIB3043-050-F6_FLI
US-10-425-114-15025

Alignment Scores:
Pred. No.:      7e-68      Length:      1231
Score:          652.00        Matches:      143
Percent Similarity: 70.45%    Conservative: 31
Best Local Similarity: 57.89% Mismatches:      53
Query Match:    53.62%        Indels:       20
DB:             13           Gaps:         8

US-10-069-527-4 (1-232) x US-10-425-114-15025 (1-1231)

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Db      264 ATGGGTGTCAGAGATTCAGTAAAGTTGATGGAAAGCCCAAGCAAGCAAGTCACT 323
QY      21 TyrSerLysArgArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAsp 40
Db      324 TACTCCAGGCAAGCAAGATTCAGTAAAGTTGATGGAAAGCCCAAGCAAGTCACT 383
QY      41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
Db      384 GCCAAGGTTTCACCTATCATGTTCTTAAACCAACAGATGATGATTAATGACCT 443
QY      61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGly---IleAspLeu 79
Db      444 GGCCCTCAGCAAAAAGATCATGATCATGATCAGAAAGACTTGGGGATTTGATCTG 503
QY      80 TTPAArgThrHisGluGlnSerMetLysAspThrLeuTTPlyLysLeuLysGluIleAsn 99
Db      504 TGGCATTTCTCAGTATGAGAAATGCTTGAAACCTTGAAAGAGCTATGATTTAAACAT 563
QY      100 LysLeuArgArgGluIleArgGlnArgLeuGlyHis-----AspLeuAsnGlyLeuSer 117
Db      564 AAGCTCAGAGACAGATTCAGGATGATGATGATGATGATGATGATGATGATGATGATG 623
QY      118 PheAspGluLeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGln 137

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Db 624 TTCGAGCACTGGCAGACTCTTGAAGAGATATGTTTCATCATAGGGAATAATCCGGA 663
QY 138 ArglyrYrHsValIlelyeThrGlnThrlysllyVallyAsnleu 157
Db 684 CGAAAGTTTCACGATCAAACTCGACATGATCTGTAGGAAAAGGTTAAAGCCTG 743
QY 158 GluGlnArgArGlyAsnMetLeuH:sglyTyrrPheAspGlnGluAlaIaGlyGluAsp 177
Db 744 AAGCAGATGAAATGGAAATCTGCTG-----CTTGAATCTGAAAGTGTGATCCAT 794
QY 178 ProGlnTyrglyTyrgluAspAsnGluGlyAspTyrgluSer----- 191
Db 795 CCACAATTTCTTTTTCACAGAT---GAAAGAGACAGAGAAATCAGCAGCAGCAGCAGCA 851
QY 192 ---AlaLeuAlaLeuSerAsnGlyAlaAsnAsnleuTyrrPhe---HisLeuHis 209
Db 852 GCACAGTGTGACTGGCCACAGGTCCTCCACCTGTATGATCTGTCTATCGACACAT 911
QY 210 ProAsnleu-----HisHieGlyGlySerSerleuGlySerSerIleThrHis 225
Db 912 TCTCATCTGAACCTTTTCTCCACCATTTCAATGAGAGAGACACCTTTAAATCAT 971
QY 226 LeuHisAspLeuArgLeuAla 232
Db 972 ---CATGACCTTCGCTTGTCT 989

RESULT 5
US-10-425-114-11957
; Sequence 11957, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 11957
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701148021_FLI
US-10-425-114-11957

Alignment Scores:
Pred. No.: 1,63e-66 Length: 1212
Score: 640.50 Matches: 142
Percent Similarity: 70.04% Conservative: 31
Best Local Similarity: 57.49% Mismatches: 55
Query Match: 52.67% Indels: 19
DB: 13 Gaps: 8

US-10-069-527-4 (1-232) x US-10-425-114-11957 (1-1212)
QY 1 MetAlaArgGlylyslleGluIleGlyLeuIleGluAsnGlnThrAsnArgGlnValThr 20
Db 232 ATGGGTCTGTGGCAAGATTGATTAAGTTGATTGATGAACCCACCAAGAGCGAATGACC 291
QY 21 TySerlyArgArgArgsnGlyIlePheIlysllyAlaGlnGluLeuThrValleuCyasp 40
Db 292 TACTCCAGGAGGAGATGATGATCTTCAAGAAAGCTCATGAATCAGTGTCTGTGTAT 351
QY 41 AlaIyValSerleuIleMetLeuSerAsnThrAsnIyMetH:sglyTyrrIleSerPro 60
Db 352 GCCAAGTTTCATCTATCATGTTCTCTAATAACAAACAATGCAATGATTAAGCCCT 411

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QY 61 ThrThrThrThrlySerMetTyrrAspAspTyrglnlyslThrMetGly---IleAspLeu 79
Db 412 GGCCTCCACACAAAAGATCATTTGATCAGATACGAAAGACTTTGGGGGATATGATCTG 471
QY 80 TPATrThrHieGluGlySerMetLyAspThrleuTyrrlysllyGluIleAsnAsn 99
Db 472 TGGCATTTCTCATGAGAAAATGCTTGAATACTTGAAGAAAGCTGAAGATATTACAT 531
QY 100 LysLeuArgArgGluIleArgGlnArgleuGlyHis-----AspLeuAsnGlyLeuSer 117
Db 532 AAGCTCGGAGACAGATACGATAGCATGTAGTGAGGCTTGGACATGACGACATGAGC 591
QY 118 PheAspGluLeuAlaSerLeuAspAspGlyMetGlnSerSerLeuAspAlaIleArgGln 137
Db 592 TTCGAGCACTCCGCACTCTTGAAGAATATGTTTATCATAGGGAATAATCCGGA 651
QY 138 ArglyrYrHsValIlelyeThrGlnThrlysllyVallyAsnleu 157
Db 652 CGAAAGTTTCACGATCAAACTCGACATGATCTGTAGGAAAAGGTTAAAGCCTG 711
QY 158 GluGlnArgArGlyAsnMetLeuH:sglyTyrrPheAspGlnGluAlaIaGlyGluAsp 177
Db 712 AAGCAGATGAAATGGAAATCTGCTGTGAATCTT-----AAGGAAAAGTGTGATCCAT 765
QY 178 ProGlnTyrglyTyrgluAspAsnGluGlyAspTyrgluSer----- 191
Db 766 CCACAATTTCTTTTTCACAGAT---GAAAGAGACAGAGAAATCAGCAGCAGCAGCA 822
QY 192 ---AlaLeuAlaLeuSerAsnGlyAlaAsnAsnleuTyrrPhe---HisLeuHis 209
Db 823 GCACAGTGTGACTGGCCACAGGTCCTCCACCTGTATGATCTGTCTATCGACACAT 882
QY 210 ProAsnleu-----HisHieGlyGlySerSerleuGlySerSerIleThrHis 225
Db 883 TCTCATCTGAACCTTTTCTCCACCATTTCAATGAGAGAGACACCTTTAAATCAT 942
QY 226 LeuHisAspLeuArgLeuAla 232
Db 943 ---CATGACCTTCGCTTGTCT 960

RESULT 6
US-10-424-599-66649
; Sequence 66649, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 66649
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_31198C.1
US-10-424-599-66649

Alignment Scores:
Pred. No.: 1,82e-65 Length: 1155
Score: 631.50 Matches: 141
Percent Similarity: 70.04% Conservative: 32
Best Local Similarity: 57.09% Mismatches: 55
Query Match: 51.93% Indels: 19
DB: 13 Gaps: 8

US-10-069-527-4 (1-232) x US-10-424-599-66649 (1-1155)

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QY      1 MetAlaArgGlyLysIleGluIleLeuIleGluValAsnGlnThrAspArgGlnValThr 20
Db      111 ATGGGTCCAGGCGAAGATGAGTAAAGTTGATTGAGAAACCCACCAAGGCAAGTCACT 170
QY      21 TySerLysArgArgAsnGlyIlePheLeuLysValGlnGluLeuThrValLeuCyAsp 40
Db      171 TACTCCAGGCGAAGAGTATGTTCTTCAAGAAAGCTCATGAACTCAAGTCTTCTGAT 230
QY      41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
Db      221 GCCAAGGTTTCACTATCATGTTCTCTMAAAACAACAGATGATGATATACAGCCT 290
QY      61 ThrThrThrThrLysSerMetCysTrpAspTyrGlnLysThrMetGlyIleAspLeu 79
Db      291 GGCTTCAGACAAAGAAAGATCATTTGATCATGATCAAGAAAGCTTTGGGGGATATTGATCTG 350
QY      80 TrpArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeuValLeuAspAsn 99
Db      351 TGGCGTTCTCACTAGAGAAATGCTTGAATACTGAAGAAAGCTGATGATATTAAACAC 410
QY      100 LysLeuValGlyArgGluIleArgGlnArgLeuGlyHis-----AspLeuAsnGlyLeuSer 117
Db      411 AAGCTCAAGAAAGCAAGATCAGGCTAGGATAGGTAGGGGTTGGACATGACAGCATGAGC 470
QY      118 PheAspGluLeuAlaSerLeuAspArgLysMetGlnSerSerLeuAspAlaIleArgGln 137
Db      471 TTCGACAGACTGCGCACTCTTGAGAGAGATTTGGTTCTTCCATAGGAAATACAGAGA 530
QY      138 ArgLysTyrHisValIleLysThrGlnThrGlnThrLysLysValLysAsnLeu 157
Db      531 CGAAAGTTCCAGCTGATCAAAACAGCACTGATACCTCAGAGAAAGGTTAAAGCTCG 590
QY      158 GluGlnArgArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaGlyGluAsp 177
Db      591 GAGCGATGATAGAGATCTGCTGCTTGAACCT-----AAGAAAGTGTGTGATTCAT 644
QY      178 ProGlnTyrGlyTyrGluAspAsnGluLysAspTyrGluSer----- 191
Db      645 CCACAAATTTCTTTGACAGAT---GAGGAGACGAGATCAGCAGCAGCAGCAGACA 701
QY      192 ---AlaLeuAlaLeuSerAsnGlyAlaAsnAsnLeuTyrThrPhe---HisLeuHisHis 209
Db      702 GCAGAGAGTTGACGCTGGCCAAACGTCCTCCACCCGTATGCAATTCGTATCAGACCAT 761
QY      210 ProAsnLeu-----HisHisGlyGlySerSerLeuGlySerSerIleThrHis 225
Db      762 TCTCATCTGACCTTTTCTCCACCACTTCTAATGAGAGAACACCTTTAAACATGAT 821
QY      226 LeuHisAspLeuArgLeuAla 232
Db      822 ---CATGACCTTCGCTTGTCT 839

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ORGANISM: Gossypium hirsutum
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(644)
OTHER INFORMATION: unsure at all n locations
US-10-021-323-8631

Alignment Scores:
Pred. No.: 1,67e-63 Length: 644
Score: 612.00 Matches: 118
Percent Similarity: 75.00% Conservative: 38
Best Local Similarity: 56.73% Mismatches: 47
Query Match: 50.33% Indels: 5
DB: 17 Gaps: 2

US-10-069-527-4 (1-232) x US-10-021-323-8631 (1-644)
QY      1 MetAlaArgGlyLysIleGluIleLeuIleGluValAsnGlnThrAspArgGlnValThr 20
Db      32 ATGGCTCGAGGAGAAATCCAGATCAAGCTGATAGAGAACTCCAGCAAGGCAAGTCAAG 91
QY      21 TySerLysArgArgAsnGlyIlePheLysValGlnGluLeuThrValLeuCyAsp 40
Db      92 TATTCCAGAGAGAAAGAAACGGTCTTTTCAAGAAAGCTAATGAACTTACAGTCTTTCGAT 151
QY      41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
Db      152 GCTAGAGTTTCATCATCATGTTTCCACTACGTAAGTAACTCCATAGATTTTACAGCCT 211
QY      61 ThrThrThrThrLysSerMetCysTrpAspTyrGlnLysThrMetGlyIleAspLeuTyr 80
Db      212 TCCACCAACAAGCAAGCAAGATTTGATGATCAGTACCAAGAAACCTTGGGGAATCGATCTCG 271
QY      81 ArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeuValLysAsnLeuLys 100
Db      272 AACCCCATATAGAGAAATGCAAGACGATTAAGCGAGTGAAGAGGTTAACAGAGAAC 331
QY      101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
Db      332 CTGGCAAAAGATTTAGAGAAAGATGCGGCACTGTTGAATGATTTGAGCATCGAAGAT 391
QY      121 LeuAlaSerLeuAspArgGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
Db      392 CTGGTGCCTTTGAGAAACAAATGAGAGAGCTGTGATCTTTTGTGTAGTAAAGTAT 451
QY      141 HisValIleLysThrGlnThrGlnThrLysLysValLysValLysAsnLeuGlnGlnArg 160
Db      452 CGGTCTCTCCAAACGATCATCTTCCAGAAAGAGTGAAGATGAGAGATG 511
QY      161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaGlyLysAspProGlnTyr 180
Db      512 CACAAATCTCTTACAT-----GAAGTGAATCCCTGAAAGATGCA---TAT 559
QY      181 GlyTyrGluAspAsnGluLysAspTyrGlnSerAlaLeuAlaLeuSerAsnGlyAlaLys 200
Db      560 GGAATTAAGTTGATGAGAGGAGATTAATGATACCTGATCGGATATCAAAATGAGAGTCC 619
QY      200 AsnLeuTyrThrPheHisLeu 207
Db      620 TCGATATTTGCTTACGCTTG 641

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RESULT 7
US-10-021-323-8631
; Sequence 8631, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Pincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 8631
; LENGTH: 644
; TYPE: DNA

```

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RESULT 8
US-10-424-599-120794
; Sequence 120794, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

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FILE REFERENCE: 38-21(53223)B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO 120794
 LENGTH: 1036
 TYPE: DNA
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_80083C.1
 US-10-424-599-120794

Alignment Scores:

Pred. No.:	2,66e-62	Length:	1036
Score:	604.50	Matches:	117
Percent Similarity:	69.47%	Conservative:	40
Best Local Similarity:	51.77%	Mismatches:	62
Query Match:	49.71%	Indels:	7
DB:	13	Gaps:	3

US-10-069-527-4 (1-232) x US-10-424-599-120794 (1-1036)

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QY 1 MetAlaArgGlyLysIleGluLeuLeuIleGluAsnGlnThrAsnArgGlnValThr 20
DB 27 ATGCTCGAGGAAAGATCCAGATCAAGAGATAGAGAACACCAACCCAGCTCAGT 86
QY 21 TySerLysArgArgGlnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAsp 40
DB 87 TATCTAAACGACCGAATGGCTTTTCAGAGGCCAACAGCTCACCGTTCTATGCGAT 146
QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerPro 60
DB 147 GCCAAGTTTCTATATATATGTTCTCCAGCATGGGAACTCCAGATGATCAAGCC 206
QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTyr 80
DB 207 TCCACCTCAACCAAGCGATCTTCGATCAGTACAGATGACTCTAGAGAGCGATCTCTG 266
QY 81 ArgThrHisGluGluSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnLys 100
DB 267 AACTCTATTCGAGAAATATGCAAGAGACTTGAAGAACTGAAGATGGAATGGAAT 326
QY 101 LeuArgArgGluIleArgGlnArgLeuGlnLysHisAspLeuAsnGlyLeuSerPheAspGlu 120
DB 327 CTTCGTAAAGGAGATTAGGACAGAGATGGAGATTTGTTGTAACATCTGGGCATGAAAGT 386
QY 121 LeuAlaSerLeuAspArgGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
DB 387 CTCAGCTCTCTTGAGAGAAATGACACAGCCGCGCAAGGTGTGCTGAGCGTAAAGT 446
QY 141 HisValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeuGluGlnArg 160
DB 447 AAGGTGATTAACAATTCAGATTGACACCCAGAGAAAAAGTTTAATACAGAAAGAAAGT 506
QY 161 ArgGlyAsnMetLeuHisGlyTyrPheAspGlnGluAlaAlaGlyLysAspProGlnTyr 180
DB 507 CACAAACAGACTCCGCGAT-----GACTTGAGTCAAAACAAAGATCCACCTTT 557
QY 181 GlyTyrGluAspAsnGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGluAlaAsn 200
DB 558 GCATTGATTAATTAAGAGAGAGATGAGCTGTGTCGATTCTCAAAATTTAGGTCCA 617
QY 201 AsnLeuTyrThrPheHisLeuHis-----HisProAsnLeuHisHisGlyLysSer 218
DB 618 CGCATGTTCGATTGACCTTACAGCCAAAGCCATCTTAGTCCCAAGCGGAGAGACA--- 674
QY 219 LeuGlySerSerIleThr 224
DB 675 ---GGCTGATCTTACC 689

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RESULT 9
 US-10-425-114-10670
 Sequence 10670, Application US/10425114

Publication No. US20040034888A1
 GENERAL INFORMATION:
 APPLICANT: Liu, Jindong
 APPLICANT: Zhou, Yinhua
 APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E
 APPLICANT: Tabaska, Jack E
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(5323)B
 CURRENT APPLICATION NUMBER: US/10/425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 10670
 LENGTH: 871
 TYPE: DNA
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: 700958586_FLI
 US-10-425-114-10670

Alignment Scores:

Pred. No.:	4,67e-59	Length:	871
Score:	576.50	Matches:	112
Percent Similarity:	68.47%	Conservative:	40
Best Local Similarity:	50.45%	Mismatches:	63
Query Match:	47.41%	Indels:	7
DB:	13	Gaps:	3

US-10-069-527-4 (1-232) x US-10-425-114-10670 (1-871)

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QY 5 LysIleGluIleLysLeuIleGluAsnGlnThrAsnArgGlnValThrTyrSerLysArg 24
DB 3 AAGATCCGAGTCAAGAGATAGAGAACACCAACCCAGGACCTTTCTTCAAAACGA 62
QY 25 ArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAspAlaLysValSer 44
DB 63 CGAATGCGCTTTTCAAGAGGCCAACAGAGTCAAGCTCCTTATGCGATGCCAAGTTTCT 122
QY 63 LeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrIleSerProThrThrThr 64
DB 123 ATTATATGTTCTCCAGACCTGGGAAACTCCACAGATGATCAAGCCCTCCACTCAACA 182
QY 65 LysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTyrArgThrHisGlu 84
DB 183 AAGCAGTTCTTCGATCAGTACCAAGATGAGCTTAGAGTCCGATCTGGAAGTCTCATTTAC 242
QY 85 GluSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnLysLysLeuArgGlu 104
DB 243 GAGATATGCAAGAACTTGAAGAACTGAAGATGGAATAGAGATCTTCGTAAGAG 302
QY 105 IleArgGlnArgGluGlnLysAspLeuAsnGlyLeuSerPheAspGluLeuAlaSerLeu 124
DB 303 ATTAGGCGAGAGATGGGAGATTGTCTGAACGATTTGGGCAATGGAAGATCCCAAGCTCTT 362
QY 125 AspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyrHisValIleLys 144
DB 363 GAGAGAGAAAGCAAGAGCCGCCAAGCTTGTCTGAACGTAAAGTAAAGTGAATACA 422
QY 145 ThrGlnThrGlnThrThrLysLysValLysAsnLeuGlnGlnArgArgGlyAsnMet 164
DB 423 AATGAGATTGACCCCAAGGAAAAAGTTTAATTAACAGAAAAAGAGTCAACAGACTC 482
QY 165 LeuHisGlyTyrPheAspGlnGluAlaAlaGlyLysAspProGlnTyrGlyTyrGluAsp 184
DB 483 CTGCGT-----GACTTGATGCAAGAGCGAAAGATCCAGCTTTTGCAATTGATGAT 533
QY 185 AsnGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGluAlaAsnLeuTyrThr 204
DB 534 AATGAGAGGAGTACGAGTCTGTGATCGATTCTCAAAATTTAGTCCACGACATGTTGCA 593
QY 205 PheHisLeuHis-----HisProAsnLeuHisHisGlyLysSerLeuGlyLysSer 222

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D	b		594 TTGAGCTTACGCGCAACCATTCTTAGTGCCAAAGCGAGCAGA-----GGCTCTGTAT	647
O	y	223 lIeThr	224	
D	b		648 CTTACC	653
<p style="text-align:center;">RESULT 10 US-10-260-238-5530</p>				
; Sequence 5530, Application US/10260238				
; Publication No. US20040016025A1				
GENERAL INFORMATION:				
APPLICANT: Budworth, Paul R.				
APPLICANT: Moushamer, Todd G.				
APPLICANT: Briggs, Steven P.				
APPLICANT: Cooper, Bret				
APPLICANT: Glazebrook, Jane				
APPLICANT: Goff, Stephen A.				
APPLICANT: Katagiri, Fumiyaki				
APPLICANT: Kreps, Joel				
APPLICANT: Provart, Nicholas				
APPLICANT: Ricke, Darrell				
APPLICANT: Zhu, Tong				
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION				
FILE REFERENCE: 60111-NP				
CURRENT APPLICATION NUMBER: US/10/260,238				
CURRENT FILING DATE: 2002-09-26				
PRIOR APPLICATION NUMBER: US 60/325,448				
PRIOR FILING DATE: 2001-09-26				
PRIOR APPLICATION NUMBER: US 60/325,277				
PRIOR FILING DATE: 2001-09-26				
PRIOR APPLICATION NUMBER: US 60/370,620				
PRIOR FILING DATE: 2002-04-04				
NUMBER OF SEQ ID NOS: 6077				
SEQ ID NO 5530				
LENGTH: 681				
TYPE: DNA				
ORGANISM: Zea mays				
US-10-260-238-5530				
Alignment Scores:				
Pred. No.:	1,85e--56	Length:	681	
Score:	553.50	Matches:	122	
Percent Similarity:	64.85%	Conservative:	33	
Best Local Similarity:	51.05%	Mismatches:	63	
Query Match:	45.52%	Indels:	21	
DB:	16	Gaps:	7	
US-10-069-527-4 (1-232) x US-10-260-238-5530 (1-681)				
O	y	1 MetalArgelylysllleglullellyslleluanglnthrshnarglnvalThr	20	
D	b	1 ATGGGGGCGCGCAAGTCAGATCAAAGCGCATGAAGGCCAACCAACCGCGAGGTACC	60	
O	y	21 TysSerlysaRgrArGaenGIYIlEPheLySLySAJaInGLueLueThrValLeUcYaSP	40	
D	b	61 TACTCCAAGCCCGCGAGCGGGAGATCAAGAAAAGCCCGGAGACTCACCGTCTCTGGAC	120	
O	y	41 AlAlayValserIeuIIemelleUserrAnthrAmLYmehchISglUTyrILeserPro	60	
D	b	121 GCCCAGGTCGCATCATCATGTCTCTCTCCACCGCGCAGTACAAGAGTCTTGACAGCCC	180	
O	y	61 ThrThrThrThrIlysSerMetTyzAsPARPyrgLnlsYThmerGIylleaSPLeutir	80	
D	b	181 GGAAACCGACATCAAAGACCATCTTGACCGGTACACAGAGGCCATCGGACCAAGCTTAG	240	
O	y	81 ArgThrHtsGlugIsuSerMetLyasPrThrLeutirPLySLeuLySGLIlaShnAnLYs	100	
D	b	241 ATCGAGCAGTATGAGMATATGCAAGCGCACGCTGAGGCATCTCAAGACATCATCTGTGT	300	
O	y	101 LeuAtgAdgGuIlleaVgInatgLeuGIynHIsAprLeandngilyLeusPhaeSPgu	120	
D	b	301 CTGGCCACAGAGATTAGGCAAAAGAGATGGGAGAGATCTGGAAGTCTGGAAGCTGAGAG	360	

Query: 121 LeuAlaSerLeuAspArgLumMetGlnSerSerLeuSpsAlaIleArgGlnArgTyr 140

Dn 361 CTGGCGCCGCCCTTCAGCAAAACGTGCAGCGGGCTCTCAGAAGAGTTCCCATAGGAAGTAC 420

Qy 141 HisValIleuSThrGlnThrGlnThrThrlsYlsYsVallyAsnLeuGlnGlnArg 160

Dd 421 CATGTGATCAGCACGACAGACTGATACTTACAAGAAAAAGTGAAAGCACTCCGACCAAGCG 480

Qy 161 ArgGlySerMetLeuHisGlyTyrPheAspGlnGluAlaIleGly-----GluAspPro 178

Dd 481 TACAGAACCTG-----CAGCAGAGCTAGAGCATCCGGAGGAGACC 522

Qy 179 GlnIleGlyTyrGluAspAsnglUgyl-----AspTyrGlnSerAlaLeuAlaLeu 195

Dd 523 GCCTTCGGATACGTGAGCAACACCGCGCCGCCCTCCGCTCGCTGCAGACGCGCGCGCGCG 582

Qy 196 SerAsnGlyAla---AasnLeuTyrThrPheHisLeu-----HisHisProAsnLeu 212

Dd 583 CTGGCGCGCGCGCCCGCGGACATGATGACCTTCGCGGTGTCGCCACGACGACCCCACTG 642

Qy 213 HisHisGlyGlySerSerLeuGlySerSerIleThrHisLeuHisAspLeuArgLeu 231

Dd 643 CAC-----GGCATGCGCTTACGCG-----TTCCACGAGCTTCGCGCTG 678

RESULT 11

US-09-732-627A-4479
; Sequence 4479, Application US/09732627A
; Publication No. US2004012338A1
GENERAL INFORMATION:
APPLICANT: Fincher, Karen L.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51770)B
CURRENT APPLICATION NUMBER: US/09/732,627A
CURRENT FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 4930
SEQ ID NO 4479
LENGTH: 498
TYPE: DNA
ORGANISM: *Gossypium hirsutum*
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(498)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3493-034-P1-M1-H12
US-09-732-627A-4479

Alignment Scores:

Pred. No.:	3,34e-54	Length: 498
Score:	533.00	Matches: 99
Percent Similarity:	81.29%	Conservative: 27
Best Local Similarity:	63.87%	Mismatches: 29
Query Match:	43.83%	Indels: 0
DB:	12	Gaps: 0

US-10-069-5227-4 (1-232) x US-09-732-627A-4479 (1-498)

Qy 1 MetaLaarGlyLyseIleGlnIleuLeuIleGluAsnGlnThrsAnArgInValThr 20

Dd 25 ATGGCTCGAGGGAMAATCCAGATCAAGCTGATAGGAATCGACCAACAGGCAAGTCAAG 84

Qy 21 TyrSerLySarGArAsnGlyIlePheLySLysAlaGlnIleuThrValIeuCyAsp 40

Dd 85 TATTGGAAGAGAAACCGTCTTTTCCAAGAAAGCTTAAGAACTTACAGTTCTTCCGAT 144

Qy 41 AlaLyValSerLeuIleVeLeuSerAsnThrAsnLyMetHisGluTyrlIsSerPro 60

Dd 145 GGTAAAGTTTCATCATCATATGTTTTCCACTACTGTAACTCCATGAGTTTATCAAGCCC 204

Qy 61 ThrTrtTrtThrLySeSerMetTyraSpApTyrgInLyVThMeGlYtlleaSpLeutrp 80

Dd 205 TCACACCAACGACCAAGCAATATGATGCTACGAGAAACCTTGGGGATTCGATCTGG 264

```
QY 81 ArgThrHisGluGluSerMetLeuSerPheThrLeuTrpLeuLeuGluLeuAsnAsnLys 100
DB 265 AACACCCACTATGAGAAAATGACAGACAGTGAAGCAGCTGAAAGAGTTAAACAGAGAC 324
QY 101 LeuAlaSerGluLeuLeuArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
DB 325 CTGCCAAGAGATTGAGAGAGAGATGGCAGCTGTTGAAATGATTTGAGATCGAAGAT 384
QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaLeuArgGlnArgLysTyr 140
DB 385 CTGTGCTGTTGGAACAAGAAATGAGAGCTCTGTCACTCTTATTCGTGATGAAAGTAT 444
QY 141 HisValIleLysThrGlnThrGlnThrThrLysLysValLys 155
DB 445 CGTGTCTCTCCAAACCAAGATGATGATCTTCAGAGAAAAAGTAGAG 489

RESULT 12
US-10-425-114-13190
; Sequence 13190, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 13190
; LENGTH: 2237
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: jC-gm102220148g09_FU1
US-10-425-114-13190

Alignment Scores:
Pred. No.: 3,57e-46 Length: 2237
Score: 474.00 Matches: 87
Percent Similarity: 80.58% Conservative: 25
Best Local Similarity: 62.59% Mismatches: 27
Query Match: 38.98% Indels: 0
DB: 13 Gaps: 0

US-10-069-527-4 (1-232) x US-10-425-114-13190 (1-2237)
QY 1 MetAlaArgGlyLysIleGluIleLeuIleGluAsnGlnThrAsnArgGlnValThr 20
DB 109 ATGGCTGAGAGAAAGATCCAGATCAAGAGATGAGAAACAAACCCAGAGGTCACT 168
QY 21 TyrSerLysArgGlnArgGlnGlyIlePheLysValGlnGlnLeuThrValLeuCysAsp 40
DB 169 TACTCTAAACGACGAGATGCGCTTTCAAGAGCCCAAGAGCTTACCGTCTCGCAT 228
QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlnLysIleAspLeuTrp 60
DB 229 GCCAAGGTTCTATTATGTTCTCCAGACTGGAAGAACTCCACAGATCACTAGCCCC 288
QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTrp 80
DB 289 TCACACCTCAACAAAGAGCTTCTCGATCAATACCAATAGATCTCGGAGATTATCTCTGG 348
QY 81 ArgThrHisGlnGlnLeuSerMetLysAspThrLeuTrpLysLeuLysGlnIleAsnAsnLys 100
DB 349 AACTCTCATTAACAGAAATGACAGAACTGGAAGAACTGAAAGAGGTGATGAGAT 408
QY 101 LeuArgArgGluLeuLeuArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
```

```
DB 409 CTTGTAAGAGAGATTAGGAGAGAAATGGAGATTGTTGTAAGCACTGGCGCATGGAAGT 468
QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaLeuArgGlnArgLys 139
DB 469 CTCACCTCTTGAAGAGAAATGACAAAGCCCGCAAGGTGTTGTAAGCGTAAAG 525

RESULT 13
US-10-424-599-120795
; Sequence 120795, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 120795
; LENGTH: 2718
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_80084C.1
US-10-424-599-120795

Alignment Scores:
Pred. No.: 1,09e-45 Length: 2718
Score: 471.00 Matches: 86
Percent Similarity: 80.58% Conservative: 26
Best Local Similarity: 61.87% Mismatches: 27
Query Match: 38.73% Indels: 0
DB: 13 Gaps: 0

US-10-069-527-4 (1-232) x US-10-424-599-120795 (1-2718)
QY 1 MetAlaArgGlyLysIleGluIleLeuIleGluAsnGlnThrAsnArgGlnValThr 20
DB 126 ATGGCTGAGAGAAAGATCCAGATCAAGAGATGAGAAACAAACCCAGAGGTCACT 185
QY 21 TyrSerLysArgGlnArgGlnGlyIlePheLysValGlnGlnLeuThrValLeuCysAsp 40
DB 186 TATCTTAAACGACGAGATGCGCTTTCAAGAGGCCCAAGAGCTCACCGTCTATGCGAT 245
QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGlnLysIleAspLeuTrp 60
DB 246 GCCAAGGTTCTATTATGTTCTCCAGACTGCGAAACTCCACAGATCACTAGCCCC 305
QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuTrp 80
DB 306 TCACCTCAACAAAGAGCTTCTCGATCAATACCAATAGATCTCGGAGATTATCTCTGG 365
QY 81 ArgThrHisGlnGlnLeuSerMetLysAspThrLeuTrpLysLeuLysGlnIleAsnAsnLys 100
DB 366 AACTCTCATTAACAGAAATGACAGAACTGGAAGAACTGAAAGAGGTGATGAGAT 425
QY 101 LeuArgArgGluLeuLeuArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
DB 426 CTGTGTAAGAGATTAGGAGAGAGATGGAGATGTTCTGAACGATCTGGGATGAGAAAT 485
QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaLeuArgGlnArgLys 139
DB 486 CTCACGCTCTTGAAGAGAAATGACAAAGCCCGCAAGGTGTTGTAAGCGTAAAG 542

RESULT 14
US-09-922-293-3294
; Sequence 3294, Application US/09922293
; Publication No. US20040123339A1
; GENERAL INFORMATION:
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APPLICANT: Comer, Timothy W.
 APPLICANT: Heck, Gregory R.
 APPLICANT: Liu, Jingsong
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 FILE REFERENCE: 16517.254
 CURRENT APPLICATION NUMBER: US/09/922,293
 PRIOR FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: US 60/067,000
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? PRIOR FILING DATE: 1998-12-11
? PRIOR APPLICATION NUMBER: US 60/113,224
? PRIOR FILING DATE: 1998-12-22
? PRIOR APPLICATION NUMBER: US 09/229,413
? PRIOR FILING DATE: 1999-01-12
? NUMBER OF SEO ID NOS: 3853
? SEO ID NO 3294
? LENGTH: 407
? TYPE: DNA
? ORGANISM: Glycine max
? US-09-922-293-3294

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 PRIOR APPLICATION NUMBER: US 60/111,981

PRIOR FILING DATE: 1998-12-11
 PRIOR APPLICATION NUMBER: US 60/113,224
 PRIOR FILING DATE: 1998-12-22
 PRIOR APPLICATION NUMBER: US 09/229,413
 PRIOR FILING DATE: 1999-01-12
 NUMBER OF SEQ ID NOS: 3853
 SEQ ID NO 14
 LENGTH: 425
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 US-09-922-293-14

Alignment Scores:
 Pred. No.: 1,466-42 Length: 425
 Score: 435.00 Matches: 84
 Percent Similarity: 76.268 Conservative: 22
 Best Local Similarity: 60.438 Mismatches: 33
 Query Match: 35.774 Indels: 0
 DB: 12 Gaps: 0

US-10-069-527-4 (1-232) x US-09-922-293-14 (1-425)

Cy 2 A1AAGGlyLysIleGluIleLysLeuIleGluAsnGlnThrAspArgGlnValThrTyr 21
 Db 2 GCGAGAGGAGAGATCCAGATCAAGAGATAGAGAACCAACACACAGACAGAGATGAGTAT 61

Cy 22 SerLysArgArgAsnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAspAla 41
 Db 62 TCAGAGAGAGAGATGCTTATTCAGAGAGACATGAGCTCAGCGTTTGATGATGCT 121

Cy 42 LysValSerLeuIleValLeuSerAsnThrAsnLysMetHisGluTyrIleSerProThr 61
 Db 122 AGCGTTTCGATTCATGTTCTCTAGCTCCACCAAGCTTCATGAGTATTCAGCCCTAAC 181

Cy 62 ThrThrThyLysSerMetTyrAspAspTyrGlnLysThrMetGlyLysAspLeuTyrArg 81
 Db 182 ACCACACAGAGAGATCGTAGTCTGACCAACTATTTTCATGATGCTGATGCGGC 241

Cy 82 ThrHisGluGlnSerMetLysAspThrLeuTyrLysLeuIleAsnAsnLysLeu 101
 Db 242 ACTCATATGAGGAGATGCAAGAAACCAAGAGAACTGTGAGACAAATGAAATCTC 301

Cy 102 ArgArgGluIleArgGlnArgLeuGlnHisAspLeuAsnGlyLeuSerThesAspGluLeu 121
 Db 302 CGAGCTCAGATCAGAGAGAGCTAGGTGATGCTTTGACAGCTTACATTCAGAGAGCTG 361

Cy 122 AlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
 Db 362 CGTCGTTTGAGATGAATGAAACACTTCAAACTGTTGCGAGCGCAAGTTC 418

Search completed: September 26, 2004, 11:29:32
 Job time: 475.861 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 26, 2004, 02:47:13; Search time 2630.89 Seconds

(without alignments)
2633.339 Million cell updates/sec

SUMMARIES

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Title: US-10-069-527-4
Perfect score: 1216
Sequence: 1 MARCKRKIKLENTNRQV.....HGGSSGSSITLHDLRLA 232
Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0
Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Command line parameters:
-MODEL=frame+2n.model -DEV=xlh
-O=/cgn2.1/USPTO-SPool/US10069527/runat.23092004.163623.5752/epd_query.fasta.1.782
-DB=EST -QFMT=fastp -SUFFIX=1st -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10069527 @CGN 1.1.3596 @runat.23092004.163623.5752 -NCPU=6 -ICPU=3
-NO MAP -LARGEDUPRY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELext=7

Database :

EST:*

- 1: em.estba:*
- 2: em.esthum:*
- 3: em.estin:*
- 4: em.estm:*
- 5: em.estcov:*
- 6: em.estpl:*
- 7: em.estpro:*
- 8: em.hic:*
- 9: gb.est1:*
- 10: gb.est2:*
- 11: gb.hic:*
- 12: gb.est3:*
- 13: gb.est4:*
- 14: gb.est5:*
- 15: em.estfun:*
- 16: em.estom:*
- 17: em.gss.hum:*
- 18: em.gss.in:*
- 19: em.gss.pln:*
- 20: em.gss.vit:*
- 21: em.gss.fun:*
- 22: em.gss.mus:*
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- 24: em.gss.pro:*
- 25: em.gss.pro:*
- 26: em.gss.pig:*
- 27: em.gss.vit:*
- 28: gb.gss1:*

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3	751	61.8	624	12	B1977629 jdl0 Old
4	700.5	57.6	710	13	B0875031 V001F01 P
5	699.5	57.5	698	10	AW737915 EST339342
6	688.5	56.6	652	12	B1924444 EST54433
7	667.5	54.9	722	9	AJ559554 AJ559554
8	666.5	54.8	762	14	CB971393 CAB10005_
9	666	54.8	697	9	AJ568191 AJ568191
10	652.5	53.7	605	13	B0877396 V033E07 P
11	652.5	53.7	757	14	AJ568207 AJ568207
12	651	53.5	727	14	CB990294 EST643802
13	646.5	53.2	800	9	AJ568199 AJ568199
14	646	53.1	692	14	CB972246 CAB10006_
15	635.5	52.3	581	13	B0880121 V041TF12
16	628.5	51.7	639	13	B0879075 V055E10 P
17	614	50.5	603	13	B0104750 fcl137_e
18	608	50.0	582	13	B0106725 fcl1070_e
19	606	49.8	588	13	B0880903 UM56TD01
20	599.5	49.3	555	12	B1924402 EST544281
21	598.5	49.2	808	14	CB947452 CAB2SG000
22	598	49.2	714	12	B1929568 EST549457
23	595	48.9	497	13	BQ104187 fc2185_e
24	581.5	47.8	590	10	AME24717 EST322662
25	580.5	47.7	605	12	B1928804 EST548693
26	580	47.7	573	12	B1955814 B1555114
27	580	47.7	575	12	B0559497 B0559497
28	565.5	46.5	623	10	AW944760 EST336810
29	563.5	46.3	576	12	B1929538 EST549427
30	560.5	46.1	567	10	AME24642 EST322587
31	560.5	46.1	717	14	CB838295 RFO2.110X
32	557.5	45.8	524	14	AW221174 EST297643
33	553.5	45.5	872	14	CD439730 ELO1N0528
34	553.5	45.5	1273	11	AJ109302 Zea_mays
35	550	45.2	685	13	B0101440 QGJ12J06_
36	549	45.1	508	9	B0878141 V043F04 P
37	549	45.1	678	9	A1485411 EST243732
38	549	45.1	608	9	A1484883 EST243146
39	542	44.6	543	12	B1928636 EST548525
40	541	44.5	552	12	B1930908 EST550797
41	540.5	44.4	642	14	CB087977 hK10F10.9
42	536.5	44.1	536	9	A1490575 EST249129
43	531	43.7	520	9	A1483797 EST249668
44	530.5	43.6	684	9	AJ559303 AJ559303
45	526	43.3	426	13	BQ106160 fc2475_e

ALIGNMENTS

RESULT 1
LOCUS CB921382
DEFINITION VVD070D08 353397 An expressed sequence tag database for abiotic
stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera
CDNA clone VVD070D08 5, mRNA sequence.
ACCESSION CB921382
VERSION CB921382.1 GI:30136044
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Db 592 GGGTATGTGATATGAAGGAGCTATCAATCT 624

RESULT 4
LOCUS BUB75031 710 bp mRNA linear EST 16-OCT-2002
DEFINITION V001F01 Populus flower cDNA library Populus balsamifera subsp. trichocarpa cDNA 5 prime, mRNA sequence.
ACCESSION BUB75031
VERSION BUB75031.1 GI:2406555
KEYWORDS EST.
SOURCE Populus balsamifera subsp. trichocarpa (Populus trichocarpa)
ORGANISM Populus balsamifera subsp. trichocarpa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid I; Malpighiales; Salicaceae; Salicaceae; Populus.
REFERENCE 1 (bases 1 to 710)
Unneberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries
JOURNAL Contact: BHALERAO RUPALI R.
Unpublished (2002)
COMMENT Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.
Location/Qualifiers
1. 710
/organism="Populus balsamifera subsp. trichocarpa"
/mol_type="mRNA"
/sub_species="trichocarpa"
/db_xref="taxon:3694"
/tissue_type="floral buds"
/clone_id="Populus flower cDNA library"
/note="Organ: flower"

ORIGIN

Alignment Scores:

Pred. No.:	5.01e-66	Length:	710
Score:	700.50	Matches:	141
Percent Similarity:	76.64%	Conservative:	23
Best Local Similarity:	65.89%	Mismatches:	43
Query Match:	57.61%	Indels:	7
DB:	13	Gaps:	2

US-10-069-527-4 (1-232) x BUB75031 (1-710)

QY 1 MetAlaargGlyLysIleGluIleLysLeuIleGluAsnGlnThrAsnArgGlnValThr 20
Db 85 ATGGGTGTGGAAAGATTGAATCAAGATGCAAAACCCCAACAGCGAAGTCACC 144
QY 21 TySerLysArgArgArgGlyIlePheLysLysAlaGlnGluLeuThrValLeuCysAsp 40
Db 145 TACCGAAGAGAAATGATATTTCACAAAGCCCAAGAACTCACTGACTTTGTGAT 204
QY 41 AlAlaValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluIleSerPro 60
Db 205 GCTAAGTCTCTTATCATCTTCTCCACACATCACTCAATAGATACATATCAATCCCC 264
QY 61 ThrThrThrThrLysSerMetCysAspAspTyrGlnLysThrMetGlyIleAspLeuTrp 80
Db 265 TCCACATCGACAAAGAGATCTAGATCAATATCAAGACGCTTGAAGCATAGTGTGTG 324
QY 81 ArgThrHisGluGluSerMetLysAspThrLeuTrpLysLeuLysGluIleAsnLys 100
Db 325 GGCACCTCAATACGAAATGCAAGACCTTGAAGAGCTGATATATCAATCAATTAAG 384
QY 101 LeuArgArgGluIleArgGlnArgLeuGlyHisAspLeuAsnGlyLeuSerPheAspGlu 120
Db 385 CTGAGCAAGAAATCAGGCGAGAGAGAGAGAGGCGCTGATGATGTGAGCATTTGAT 444

QY 121 LeuAlaSerLeuAspAspGluMetGluSerLeuAspAlaIleArgGlnArgLysTyr 140
Db 445 CTGGCGGCTTGTACCAACATATGACTGAACTGATGGTGTGCGGACGAAAGTAC 504
QY 141 HisValIleLysThrGlnThrGluThrThrLysLysLysValLysAsnLeuGluIleArg 160
Db 505 CATGTGATCAAAACCAAAACGAAACCTACAGAAAGAGGTGAAGATTATGAGAGAGA 564
QY 161 ArgGluAsnMetLeuHisGlyTyrPheAspGlnGluIleAlaGlyLysAspProGluTyr 180
Db 565 CATGAAACCTCTTATGGAATAT-----GAGCAAAACTAGAGGATCGACAGTAT 615
QY 181 GlyTyrGluAspAsnGluGlyAspTyrGluSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
Db 616 GGTATAGTGAACAAAT-----GAACTGTGTGTGACCTTCGAAATGGGCTTCC 663
QY 201 ArgLeuTyrThrPheHisLeuHisIleProAsnLeuHisHis 214
Db 664 AACCTTATGCAATTCGCTGCATCAACGAGCAACACACAC 705

RESULT 5
LOCUS AM737915 698 bp mRNA linear EST 18-MAY-2001
DEFINITION EST339342 tomato flower buds, anthesis, Cornell University Lycopersicon esculentum cDNA clone CT04121 5', mRNA sequence.
ACCESSION AM737915
VERSION AM737915.1 GI:7646860
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE 1 (bases 1 to 698)
van der Hoeven, R.S., Bezzerides, J.L., Matern, A.L., Holt, I.E., Liang, F., Hansen, T.S., Craven, M.B., Bowman, C.L., Roming, C.M., Nieman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue, anthesis
Unpublished (1999)
CONTACT: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.
Location/Qualifiers
1. 698
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/db_xref="taxon:4081"
/clone="CT04121"
/tissue_type="flower"
/dev_stage="anthesis"
/clone_id="tomato flower buds, anthesis, Cornell University"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Tanksley; flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA496). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."

ORIGIN

Alignment Scores:

Pred. No.:	6.29e-66	Length:	698
Score:	699.50	Matches:	140
Percent Similarity:	72.84%	Conservative:	29
Best Local Similarity:	60.34%	Mismatches:	52
Query Match:	57.52%	Indels:	11
DB:	10	Gaps:	4

US-10-069-527-4 (1-232) x AM737915 (1-698)

Alignment Scores:

Pred. No.: 2,866-62 Length: 762
 Score: 666.50 Matches: 134
 Percent Similarity: 73.01% Conservative: 31
 Best Local Similarity: 59.29% Mismatches: 54
 Query Match: 54.81% Indels: 7
 DB: 14 Gaps: 3

US-10-069-527-4 (1-232) x CB971393 (1-762)

QY 1 MetAlaArgGlyLysIleGluIleLeuIleGluAsnGlnThrAsnArgGlnValThr 20
 Db 10 ATGGCTAGAGGAAGATTGAGTCAAGAGATGAGAACTCGACGAAACAGGCAAGCTACCC 69
 QY 21 TySerLysArgGlnGlnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCyAsp 40
 Db 70 TACTCCAGAGAGACGAATGATGATCTTCAAGAGGCGCAGTGAAGTCTGCTTGTGAT 129
 QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrlSerPro 60
 Db 130 GCTAAGCTTTCTATCATCTGCTCTCCAGTACTGAGAAAGCTCCATGATACATCAGCCCT 189
 QY 61 ThrThrThrThrLysSerMetTyrlAspAspTyrlGlnLysThrMetGlyIleAspLeuTrp 80
 Db 190 TCCACTACACGAAACAAATATTTGATGATCAGTACCGAAGACCTGAGGATCTATGG 249
 QY 81 ArgThrHisGluGlnSerMetLysAspThrLeuTrpLysLeuGluIleAsnAsnLys 100
 Db 250 AGCTATCACTATGAGAGATGCAAGAAACCTGAAAGAACTGAAAGATGTAACAAGAT 309
 QY 101 LeuArgArgGlnIleArgGlnArgLeuGlnLysHisAspLeuAsnGlyLeuSerPheAspGln 120
 Db 310 CTCAGAGAGGAGATAGGACAGAGATGGGTGAACATTTGACGATTTGACGCTTGAGGAA 369
 QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTrp 140
 Db 370 CTGCGAGATCTTGAAACAGAGATGAGAGATCTTTGAAAGATGGTTCGATAGAGATAC 429
 QY 141 HisValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeuGlnArg 160
 Db 430 CAGGAGATCAATTAACATGATGAACCTTCAAGAAAGATGAGAGATGAGAAACAATA 489
 QY 161 ArgLysAsnMetLeuHisGlyTyrlPheAspGlnGlnAlaGlyLysAspProGlnTrp 180
 Db 490 CACAAAATCTCTCCATGATGAATTT-----GATGACAGGACAGAGATCAATATCTAT 540
 QY 181 GlyTyrlGlnAspAsnGluGlyAspTyrlGlnSerAlaLeuAlaLeuSerAsnGlyValAsn 200
 Db 541 GGGCTAGTGCACATGAGGGGATTAACAACTGTTCTTGATTTCTCAATGGAAGCTCT 600
 QY 201 AsnLeuTyrlThrPheHisLeu-----HisHisProAsnLeuHisHisGlyLysSer 218
 Db 601 CCGGATATTGCCCTAAGCTTGAGAGCTTAACCGCCTAATGATCTTCACTCGGGT----- 654
 QY 219 LeuGlySerSerIleThr 224
 Db 655 GTGGGCTCTGATTGACC 672
 RESULT 9
 AJ568191 697 bp mRNA linear EST 28-JUN-2003
 LOCUS AJ568191 Antirrhinum majus library (Stueber K) Antirrhinum majus
 DEFINITION CDNA clone zeeho13a, mRNA sequence.
 ACCESSION AJ568191 GI:33294080
 VERSION AJ568191.1 GI:33294080
 KEYWORDS EST.
 SOURCE Antirrhinum majus (snappedragon)
 ORGANISM Antirrhinum majus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Lamiales; Antirrhinaceae; Antirrhineae;
 Antirrhinum.
 REFERENCE 1 (bases 1 to 697)

AUTHORS

Stueber, K. and Schwarz-Sommer, Z.
 Antirrhinum majus EST collection (Stueber, K. and Schwarz-Sommer, Z.)
 Unpublished (2003)
 JOURNAL
 COMMENT Contact: Stueber K
 Molecular Plant Genetics
 MPI fuer Zuechtungsforchung
 Carl-von-Linne Weg 10, D-50829, Germany.
 location/Qualifiers

FEATURES

Source

1..697
 /organism="Antirrhinum majus"
 /mol_type="mRNA"
 /db_xref="taxon:4151"
 /clone="zeeho13a"
 /clone_1ib="Antirrhinum majus library (Stueber K)"

ORIGIN

Alignment Scores:

Pred. No.: 2,866-62 Length: 697
 Score: 666.00 Matches: 126
 Percent Similarity: 73.30% Conservative: 36
 Best Local Similarity: 57.01% Mismatches: 53
 Query Match: 54.77% Indels: 6
 DB: 9 Gaps: 2

US-10-069-527-4 (1-232) x AJ568191 (1-697)

QY 1 MetAlaArgGlyLysIleGluIleLeuIleGluAsnGlnThrAsnArgGlnValThr 20
 Db 38 ATGGCTAGAGGAAGATTGAGTCAAGAGATGAGAACTCGACGAAACAGGCAAGCTACCC 97
 QY 21 TySerLysArgGlnGlnGlyIlePheLysLysAlaGlnGluLeuThrValLeuCyAsp 40
 Db 98 TACTCCAGAGAGAGATGATGATCTTCAAGAGGCGCAGTGAAGTCTGCTTGTGAT 157
 QY 41 AlaLysValSerLeuIleMetLeuSerAsnThrAsnLysMetHisGluTyrlSerPro 60
 Db 158 GCTAAGCTTTCTATCATCTGCTCTCCAGTACTGAGAAAGCTCCATGATACATCAGCCCA 217
 QY 61 ThrThrThrThrLysSerMetTyrlAspAspTyrlGlnLysThrMetGlyIleAspLeuTrp 80
 Db 218 ACAAGTGCAGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 277
 QY 81 ArgThrHisGluGlnSerMetLysAspThrLeuTrpLysLeuGluIleAsnAsnLys 100
 Db 278 AGCTACACTATGAGAGAAATGCAAGAGCACTTGAGAGAACTGAATAGGTCAACAGAAAT 337
 QY 101 LeuArgArgGlnIleArgGlnArgLeuGlnLysHisAspLeuAsnGlyLeuSerPheAspGln 120
 Db 338 CTAGAGAGGAGATGACGAGAGAGATGGGTGAACATTTGACGATTTGACGCTTGAGGAA 397
 QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTrp 140
 Db 398 ATTTGAATCTTATTAAGACATGATGAATCTCTCAAGCTCAATTTGTAAGAAAGATAC 457
 QY 141 HisValIleLysThrGlnThrGlnThrThrLysLysValLysAsnLeuGlnArg 160
 Db 458 AAGATCACTGATACAGAGATGACACGAGAAAGAAAGGTTCGAAATGTAAGAAATA 517
 QY 161 ArgGlyAsnMetLeuHisGlyTyrlPheAspGlnGlnAlaGlyLysAspProGlnTrp 180
 Db 518 CACAGAAACCTGCTG-----CTTGAATTTGATGACAGAGAGATCCACACTTT 568
 QY 181 GlyTyrlGlnAspAsnGluGlyAspTyrlGlnSerAlaLeuAlaLeuSerAsnGlyValAsn 200
 Db 569 GGAATGATGATATAGAGGTGATTAATTCCTGCTTGGTTCCCAATGAGGGCCT 628
 QY 201 AsnLeuTyrlThrPheHisLeu-----HisHisProAsnLeuHisHisGlyLysSer 217
 Db 629 CGATATAGCCCTAGAGCTCCCGACATATACATCCACATCTTCAACAGCGAGGGGGC 688
 QY 218 Ser 218
 Db 689 TCT 691

Db		241	ACAACCTGGCAAAAGCAGTATTTCATGCATGATCCAGAAAGCGCGTTGAGATTGATCTATGAC	300
Oy		81	ArgrthrHtsGLuglUserMetLysaspHrLeutPrybLeyuSgJullEasrAsnlys	100
Db		301	AGCTCACACTGTAGAAAATAATGCAAGACCTTGAAAGAAAGCTGAATAGATCAACGGAAT	360
Oy		101	LeuAArgAGJullLeArgJlnArgLeuGlYHisAePLeuAsnGLYleuserPheaspGu	120
Db		361	CTGAGGAGAGGAGATCAGGCCAAAGAATGGGTAGACCTTGAAAGCATCTGGGCTACGACACA	420
Oy		121	LeuAseRLeuAspAspGLUmetGlnSerSerLeuAspAlaIleArgJlnArgLysTy	140
Db		421	ATTGGAATCTTATTGAAGACATGATTAATCTTCCAAGCTCATTCGTGAAAGAAAGTAC	480
Oy		141	HIsValIleYsThGIThrGluThrTrhLybSLysVallYeAsnLeuGLUGlnArg	160
Db		481	AAAGTCATCAGTAAACCAGATGCACACCGAAGAAAAAGTTAGAAATCTTGAAATAATA	540
Oy		161	ArgGLyaMetLeuHiGLYTyrPheAspGlnGluAlaAlaGLYlunAspProGlnTy	180
Db		541	CACAGAAACCTGGTG-----CTTGAATTTGATGACAGAGAGAGATTCACACACTT	591
Oy		181	GlyTYrGLuaBpaAsGLUGLYAspTYrGLUsErAlaLeuAlaLeuSerAsnGLYlaasn	200
Db		592	GGATTAGTTGATAAAGTAAGTAGATTAATTCGTTCCTTGTTCCCAATAGAGGCGCT	651
Oy		201	AsnLeutyTYrThrPheHisLeu-----HisHsProAsnLeuHHisGLY---GLY	216
Db		652	CGTAAATACGGCCCTACGGCTCCCGCACTAATACCATCTCAGCTTCAACAGCGGAAGGCG	711
Oy		217	SerSerLeu 219	
Db		712	TCTGATCTC 720	
RESULT 12				
LOCUS	CA990294			
DEFINITION	BSf643802 GESD Medicago truncatula cDNA clone GESD-28M21, mRNA			
VERSION	CA990294			
KEYWORDS	CA990294.1 GI:27523188			
SOURCE	EST.			
ORGANISM	Medicago truncatula (barrel medic)			
	Medicago truncatula			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;			
	Medicago.			
REFERENCE	1 (bases 1 to 727)			
AUTHORS	Grusak,M.A., Samac,D.A., Town,C.D., Van Aken,S., Utterback,T.,			
	Cheung,F. and Frisner,C.M.			
TITLE	More ESTs from developing reproductive tissues of Medicago			
JOURNAL	truncatula			
COMMENT	Unpublished (2002)			
	Contact: Grusak, M.A.			
	USDA/ARS Children's Nutrition Research Center			
	Baylor College of Medicine			
	1100 Bates Street, Houston, TX 77030-2600, USA			
	Tel: 713 798 7044			
	Fax: 713 798 7078			
	Email: mgrusak@bcm.tmc.edu			
	TIGR sequence name: MTPBS83YK			
	More information is available at: www.medicago.org			
FEATURES	Seq primer: SKmod (CTA GAA CTA gtc gat CC).			
source	Location/Qualifiers			
	1..727			
	/organism="Medicago truncatula"			
	/mol_type="mRNA"			
	/cultivar="A17"			
	/db_xref="taxon:3880"			
	/clone="GESD-28M21"			
	/tissue_type="immature seeds"			
	/dev_stage="Immature seeds, 11 to 19 days after			

pollination"
/clone.lib="GSDS"
/note=Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Immature seeds, collected from pods ranging in age
from 11 to 19 days after pollination, were harvested from
greenhouse-grown plants. Seeds were removed and
separated from pod walls and were immediately frozen in
liquid nitrogen. Seeds throughout the age range were
pooled for mRNA extraction. cDNA was prepared from polyA⁺
enriched RNA. The cDNA was directionally ligated into
the Zipap XR vector from Stratagene and packaged using
GigaPack III Gold packaging extracts. Plasmids containing
cDNA inserts were excised from the recombinant lambda-Zap
phage using Ex-assist helper phage and propagated in
XOHR cells."

DB		661	CACCATGGAGAGAAGTA	681	
RESULT 13					
AJ568199					
LOCUS					
DEFINITION	AJ568199	Antirrhinum majus library (Stueber K)	Antirrhinum majus		
CDNA clone zschoc2, mRNA sequence.					
AJ568199					
VERSION	AJ568199.1	GI:33294088			
KEYWORDS	EST				
SOURCE	Antirrhinum majus (snapdragon)				
ORGANISM	Antirrhinum majus				
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
asterids; lamids; Lamiales; Antirrhinaceae; Antirrhineae;					
Antirrhinum.					
REFERENCE	1 (bases 1 to 800)				
AUTHORS	Stueber, K. and Schwarz-Sommer, Z.				
TITLE	Antirrhinum majus EST collection (Stueber, K. and Schwarz-Sommer, Z.)				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Stueber K Molecular Plant Genetics MPI fuer Zuechtungsforchung Carl-von-Linne Weg 10, D-50829, Germany. Location/Qualifiers 1. 800 /organism="Antirrhinum majus" /mol_type="mRNA" /db_xref="taxon:4151" /clone="zschoc2" /clone_id="Antirrhinum majus library (Stueber K)"				
FEATURES					
Source					
Alignment Scores:					
Pred. No.:	4.68e-60	Length:	800		
Score:	646.50	Matches:	127		
Percent Similarity:	72.77%	Conservative:	36		
Best Local Similarity:	56.70%	Mismatches:	53		
Query Match:	53.17%	Indels:	8		
Gaps:	9	Gaps:	3		
US-10-069-527-4 (1-232) x AJ568199 (1-800)					
OY	1	MetAlAAgG-GlyIysIlleGlInUlleLeuLlEgluAenGlnThrAsnArgGlnValTh	20		
DB	61	ATGGCTCAGGGGAAGATCCAGATTAAAGATAGAGAACCAAAACAAGCGAGGTAC	120		
OY	20	rTySerLySArGARaEnGlyIlePheLybLYsaIagInGUleuthrValleucySas	40		
DB	121	CTACTCCAAAGAGAAGAAATGGTTTGTTCAGAAAGCACAGAGCTCTGTGTTCTGTGGA	180		
OY	40	pAlalYSaIseerleuileMeleuseSerAsnthrasnlySMethISglUTyrIIesErPr	60		
DB	181	TGCTAAATTTCCATTATCATGATGATCCAGATCTCAGAGCTTCAGCAATACATCAGGCC	240		
OY	60	oThTrThrThrlyvserSemetyrZrAspTYrGlnlysrHmetGylilEaspLeutr	80		
DB	241	AACAACtccGACAAAGcAGTtAtTCAGtTCAGAgGcCGTtgAGAgTtGATCTATG	300		
OY	80	pArYgThrHisGlUGuSeRmetLySaSPfThreutTpIlysLeuYsgIuIleaSnly	100		
DB	301	GAGCTCACACATATGAGAAATATGCAAAGACACTTGAAAGAGCTGATGACATCAGAGAA	360		
OY	100	sleuArARgGluIleargGlnargLeuG HIIsApSpuenSGnGlyLeuSerpheASpGL	120		
DB	361	TCTGGGGGGAGATCAGGCAAAGAGATGGTGAGAGCTTGAAACGATCTGGGCTACGAACA	420		
OY	120	uLeuAlaserDeuSpaSpGluMetGInserSerDeuSpaIaIlearGlnArglySTY	140		
DB	421	AATGTGATCTTATTGTAAGACATGGATAACTCTCTCAAGCTCATGTGTAAGAAAGTA	480		
OY	140	rHisValIleySrHrgInthrGlnThrThrlYelyelYsallySaenLeuGluGlnAr	160		

Alignment Scores:

```
Dp      481 CAAAGTCATCAGTACCAAGATCGAACACCAGACAAGAAAAAGGTTTAGAATGTGAAGAANAAT 540
Qy      160 gArGcGlYasMwEtLeuHrSgLYrrPheAspGInGUAlAlaIaGLYlAsPProGIntY 180
Db      541 AACAGAAAACCTGGTG-----CTTAGATTGACCAAGAGAGAGATCCACTT 591
Qy      180 rGlyTrIGLUsPasnGInGIYaSPryrGLUsErALeUlaLeuAsErnGcIyaLaAs 200
Db      592 TGAATTAGTTGATATATAGAAGGTGATTAATTCGTCTCGTTCCTGCCAATAAGAGGGCC 651
Qy      200 nAsnLeuTyThrrPheHISleU-----HisHISProAsnLeuHrSHrSGLy---G1 216
Db      652 TCGrATATATGCccCTTAAGCcTCCGAGCTAATCACCATCTCACTTCACAGCGGAGGGG 711
Qy      216 YSerSerLeu 219
Db      712 CTCGTGATCTC 721
```

RESULT 14
CB972246 CB972246
LOCUS
DEFINITION CB972246 692 bp mRNA linear EST 30-APR-2003
CBAB10006_Ia_Fa_D07 Cabernet Sauvignon Flower Pre-bloom - CAB1 Vitis
vinifera cDNA clone CBAB10006_Ia_Fa_D07 5', mRNA sequence.
CB972246
VERSION CB972246.1 GI:30256403
KEYWORDS
EST,
Vitis vinifera
ORGANISM Vitis vinifera
SOURCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
1 (bases 1 to 692)
Goed da Silva,F., Iandolo,A., Lim,H., Baek,J., Jones,K. and Cook,D.
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drccook@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.
Location/Qualifiers
1..692
/organism="Vitis vinifera"
/mol_type="mRNA"
/culivar="Cabernet Sauvignon"
/db_xref="taxon:29760"
/clone="CAB10006_Ia_Fa_D07"
/sex="Hermaprodite"
/dev_stage="Pre-bloom"
/lab_host="DHSalpa"
/note="Organ: Flower - Pre-bloom; Vector: pDNK; Site_1:
Site_2: Still, CAB1 is a cDNA library of Vitis
vinifera cv. 'Cabernet Sauvignon' Clone 8 flowers. Samples
were collected approximately eleven days before onset of
bloom (clusters at this stage were fully developed and
flowers with calyptras or caps still attached). Sampled
vines were located at the University of California, Davis,
Experimental Vineyard. cDNAs were made by oligo-dt priming
and directionally cloned. 5' and 3' adaptors were used in
cloning as follows:
5'-AAGCAGGTGATACACGACAGATGGCCATTACGCCGGG-3' and
5'-ATTCTAGCGCCAGCGCGCCGACATG-dr(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 Kb size fraction."

Pred. No.: 4,346-60 Length: 692
 Score: 646.00 Matches: 130
 Percent Similarity: 73.15% Conservative: 28
 Best Local Similarity: 60.15% Mismatches: 52
 Query Match: 53.12% Indels: 6
 DB: 14 Gaps: 3

US-10-069-527-4 (1-232) x CB972246 (1-692)

QY 1 MetAlaAGGlyLyIleGluIleLysLeuIleGluAengIlnThraArgIlnValThr 20
 Db 51 AGGCTAAGGAGAAATGAGATCAAGAGATGAGAACTGACCAAGACGAGCTCC 110
 QY 21 TysSerLysArgArgAsnGlyIlePheLysLysAlaIngIlnLeuThrValLeuCysAsp 40
 Db 111 TACTCCAGAGACGAAATGCTATCTTCAAGAAAGCCATGAACTACCTGTTCTTGAT 170
 QY 41 AlAlaLysValSerLeuIleMetLeuSerAsnThraSerMetHisGlyTyrIleSerPro 60
 Db 171 GCTAAGGTTTCTATCATCATGCTCTCCAGTACTGGAAGCTCCATGAAATCATCAGCCCT 230
 QY 61 ThrThrThrThrLysSerMetTyrAspAspTyrGlnLysThrMetGlyIleAspLeuThr 80
 Db 231 TCCACTACACGAAACAAATATTGATGATCACTGACAAACCTGAGAGTGGATCTATGG 290
 QY 81 ArgThrHisGluGlnSerMetLysAspThrLeuTyrLysLeuLysGluIleAsnAsnLys 100
 Db 291 AGCTATCACTATGAGAGATGCAAGAAACCTGGAAGAACTGAAAGATGAGCAAGAT 350
 QY 101 LeuAlaGArgGluIleArgGlnArgLeuGlnHisAspLeuAsnGlyLeuSerPheAspGlu 120
 Db 351 CTCAGAGAGAGATTAAGGAGAGATGGGTGAACATTTGACGATTTAGGCTGAGAGAA 410
 QY 121 LeuAlaSerLeuAspAspGluMetGlnSerSerLeuAspAlaIleArgGlnArgLysTyr 140
 Db 411 CTGGCAGATCTTGAACAGAGATGAGAGATCTTTGAAGATGGTTCGATAGAGAGATC 470
 QY 141 HisValIleLysThrGlnThrGlnThrLysLysLysValLysAsnLeuGlnArg 160
 Db 471 CAGGTGATCAATATATCAAGTTGAACTTTCAGAAAGACGTAAGAGATGGAACAATA 530
 QY 161 ArgGlnAsnMetLeuHisGlyTyrPheAspGlnGlnIleAlaGlyLysAspProGlnTyr 180
 Db 531 CACAAAAATCTCTCATGAATTT-----GATGCAAGGAGACAGATCAATTTCTAT 581
 QY 181 GlyTyrGlnAspAsnGlnGlyAspTyrGlnSerAlaLeuAlaLeuSerAsnGlyAlaAsn 200
 Db 582 GGGCTAGTGAACAATGAGAGGAGATTAAGAATCTGTTGATCTTCAATGAGAGCTCT 641
 QY 201 AsnLeuTyrThrPheHisLeu-----HisHisProAsn---LeuHis 213
 Db 642 CCGGATATTGCCCTAAGCTTGACGCTGAGACGCTTAATGATCTTTCAC 689

RESULT 15

BU880121 581 bp mRNA linear EST 16-OCT-2002

LOCUS BU880121 Populus flower cDNA library Populus balsamifera subsp.

DEFINITION trichocarpa cDNA 5 prime, mRNA sequence.

ACCESSION BU880121 GI:24071645

VERSION BU880121.1

KEYWORDS EST.

SOURCE Populus balsamifera subsp. trichocarpa (Populus trichocarpa)

ORGANISM Populus balsamifera subsp. trichocarpa

REFERENCE 1 (bases 1 to 581)

1 (bases 1 to 581)

1 (bases 1 to 581)

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1 (bases 1 to 581)

1 (bases 1 to 581)

1 (bases 1 to 581)

1 (bases 1 to 581)

1 (bases 1 to 581)

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 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.
 Location/Qualifiers

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 4,776-59 Length: 581
 Score: 635.50 Matches: 128
 Percent Similarity: 76.26% Conservative: 23
 Best Local Similarity: 64.65% Mismatches: 40
 Query Match: 52.26% Indels: 7
 DB: 13 Gaps: 2

US-10-069-527-4 (1-232) x BU880121 (1-581)

QY 12 GluAsnGlnThrAsnArgGlnValThrTyrSerLysArgArgAsnGlyIlePheLysLys 31
 Db 4 AAAAAGCCCAAAACAGCAAGCAAGTCACTACTCAAGAAAGAAATGATTTTCAAGAAA 63
 QY 32 AlGlnGlnLeuThrValLeuCysAspAlaLysValSerLeuIleMetLeuSerAsnThr 51
 Db 64 GCCCAAGAACTCACTGACTGTTGATGCTGAAGTCTCTTCAATGTTCTCCAACT 123
 QY 52 AsnLysMetHisGlyTyrIleSerProThrThrThrLysSerMetTyrAspAspTyr 71
 Db 124 AACAACTCAATAGATGATTAAGCTTCACTCCATCACTCAACAAAGAAATCTTCATAT 183
 QY 72 GlnLysThrMetGlyIleAspLeuTyrArgThrHisGluGlnSerMetLysAspThrLeu 91
 Db 184 CAGAGAGCTTGAAGCTTAAGTCTGTGGGGGCACTCAATAGAGAAATGCAAGAGCACTTG 243
 QY 92 TrpLysLeuLysGlnLysAsnLysLeuAsnLysLeuAsnLysLeuAsnLysLeuAsn 111
 Db 244 AGAAGCTGATATATATCAATCAATGAAGCTGAGCAAGAAATCGGAGAGAGAGAGAG 303
 QY 112 AspLeuAsnGlyLeuSerPheAspGlnLeuAlaSerLeuAspAspGluMetGlnSer 131
 Db 304 GGCCTGATGATGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 363
 QY 132 LeuAspAlaIleArgGlnArgLysTyrHisValIleLysThrGlnThrGlnThrLys 151
 Db 364 TTGAATGGTGTGGTGGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 423
 QY 152 LysLysValLysAsnLeuGlnGlnArgGlnArgGlnArgGlnArgGlnArgGlnArgGln 171
 Db 424 AAGAGGTGAAGATTTAGAGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 474
 QY 172 GluAlaAlaGlyLysAspProGlnTyrGlyTyrGlnAspAsnGlnGlyAspTyrGln 191
 Db 475 GAAGCAAACTAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 522
 QY 192 AlaLeuAlaLeuSerAsnGlnGlnArgGlnArgGlnArgGlnArgGlnArgGlnArg 209
 Db 523 GCTGTGCACTTGCATAATGGGGGCTTCAACCTTATGATCCGCTGATCAG 576

Search completed: September 26, 2004, 07:03:49
 Job time: 2634.89 secs


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PT primer_bind /label= PCR primer_P4_binding_site
PT primer_bind /tag= f
PT primer_bind /label= PCR primer_P2_binding_site
PT primer_bind complement(770..751)
PT primer_bind /tag= g
PT primer_bind /label= PCR primer_P7_binding_site
PT primer_bind complement(818..840)
PT primer_bind /tag= h
PT primer_bind /label= PCR primer_P6_binding_site
PN M0200117334-A1.
PD 15-MAR-2001.
PF 07-SEP-2000; 2000WO-N2000176.
PX 07-SEP-1999; 99NZ-00337688.
PX (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.
PX Yao J, Morris BA;
PI WPI; 2001-235145/24.
DR P-PSDB; AA00186.
XX The sequence encodes Granny Smith apple MdPI. The invention concerns a
XX fruiting plant that has been genetically modified so that it does not
XX functionally express the MdPI or MdAP3 peptide, producing seedless
XX fruits. The DNA constructs encoding non-functional variants of MdPI/MdAP3
XX may be used to transform fruiting plants, specifically apple and pear.
XX The polynucleotides may be used in modulating, reducing or eliminating
XX seed-bearing capacity in fruiting plants, used in horticulture, and in
XX breeding programmes to monitor the progress in breeding a stable seedless
XX fruiting plant. The polynucleotides may also be used in programmes for
XX identifying nucleic acid variants from fruiting plants. They can be used
XX for pre-selecting plants (mutated in MdPI, MdAP3 or their equivalents),
XX for use in an accelerated breeding programme to produce seedless fruit.
XX They may also be used in designing probes and primers for MdPI or MdAP3,
XX or their variants. The seedless fruiting plant is more convenient than
XX seeded fruit since these can be cropped without pollination, reducing
XX dependence on bees, pollinator varieties and warm weather at flowering.
XX The absence of pollen is also advantageous to alleviate environmental
XX concerns regarding the transfer of transgenes to non-transgenic by cross
XX pollination. Seedless cultivars can also avoid or reduce biennial bearing
XX tendencies that have been attributed to the inhibition of flower bud
XX formation by developing seeds and are less susceptible to codling moth
XX compared to seeded fruit. (Updated on 11-SEP-2003 to standardise OS
XX field)
XX
SQ Sequence 868 BP, 296 A, 152 C, 208 G, 212 T, 0 U, 0 Other:

Alignment Scores:
Pred. No.: 3,76e-105 Length: 868
Score: 1103.00 Matches: 215
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-069-527-2 (1-215) x AA00103 (1-868)
QY 1 MetGlyArgGlyIysValGluIleuYargGluAsnSerSerAsnArgGlnValThr 20
Db 1 ATGGGACGTGGGAGGTGAGATCAAGAGATTGAACCTCAAGTAAAGGAGGAGGAC 60
QY 21 TySerIysArgArgAsnGlyIleIleIysIysAlaIysGluIleThrValLeuGysasp 40

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Db 61 TACTCCAGAGGAGGAGATGGATTATCAAGAGGCAAGAGAGATCACTGTTCTATGTGAT 120
QY 41 AlAlaYalSerIleuIleIleYrSerSerSergLYLysMetValGluTYrCysSerPro 60
Db 121 GCTAAGTATCTCTTATTCATTATTTCTAGCTCGGAGAGTGGTTGAATACAGCACCCCT 180
QY 61 SerThrThrLeuThrGluIleLeuAspIleTYrHisGlyGlnSerIlyIysIleuTrp 80
Db 181 TCAACTACGCTGACAGAAATCTTGACCAATATACAGACATGGAACATCTGGAGAAAGTTGTGG 240
QY 81 AspAlaIysHisGluIleuSerAsnGluValAspArgValIysIysAspAsnAspSer 100
Db 241 GATGCTAGACATGAGAACCTCAGCAATGAGTGAATGATGATGATGAGAAAGCATGACAGC 300
QY 101 MetGlnValIleuLeuArgHisIleuLYSGlyGluAspIleThrSerIleuSerHisValGlu 120
Db 301 ATGCAAGTACAGGCTCAGGCAATCTGAAAGGAGAGACATACACATGTAACCATGTAGAG 360
QY 121 LeuMetAlaLeuGluGluIleuAlaLeuGluAsnGlyIleuThrSerIleArgAspIysGlnSer 140
Db 361 CTGATGACCTTAAAGAGAGCACTTGAAATAGCCTTACAAAGTATCCGGGACAAAGCTGC 420
QY 141 LysPheValAspMetMetArgAspAsnGlyLYSAlaLeuGluAspGluAsnLYSArgLeu 160
Db 421 AAGTTCGTGACATGATGAGAGCAATGGAAGGCACTGAGAGATGAGATTAAGCCCTC 480
QY 161 ThrTYrGluLeuGluIlySGlnGlnGluMetLYSAlaLeuGluAsnValArgAsnMetGlu 180
Db 481 ACTTATAGCTGCAAAAACACAGAGATGAAATTAAGAGAGATGTGAAAACATGGA 540
QY 181 AsnGlyTYrHisGlnArgGlnLeuGluAsnTYrAsnAsnAsnGlnGlnIleProPhe 200
Db 541 AATGGATATCATCAGAGGACGTGGGGAACCTACAAACACACAGACAGATATACCTTTT 600
QY 201 AlAlaPheArgValGlnProIleGlnProAsnLeuGlnGlnArgIle 215
Db 601 GCTTCGCGTGACGCTATTCAGCCAAATCTCAGAGAGATC 645

RESULT 2
AA05089 standard; cDNA; 780 BP.
ID AA05089;
AC AA05089;
XX 16-OCT-2003 (revised)
XX 25-MAR-2003 (revised)
XX 25-JUN-1994 (first entry)
DE fbp1 cDNA for reverse genetic techniques.
XX
XX Flower; morphology; petals; MADS box protein; toxin gene; insect;
XX resistance; Frankliniella occidentalis; plant; ss.
XX
XX Pecunia x hybrida.
XX
XX Key Location/Qualifiers
XX primer_bind 8..22
XX primer_bind /*tag= a
XX primer_bind /note= "PCR primer"
XX primer_bind 731..753
XX primer_bind /*tag= b
XX primer_bind /note= "PCR primer"

W09400582-A2.
EN 06-JAN-1994.
XX
XX 07-JUN-1993; 93WO-NL000121.
XX
XX 30-JUN-1992; 92EP-00201951.
XX
XX (CPRO-) CPRO-DLO CENT PLANT BREEDING & REPRODUCT.

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XX
PI Van Tunen AJ, Mollena C, Angenent GC, Dons JWM,
XX
DR WPI: 1994-026218/03.
DR P-PSDB; AAR46555.
XX
PT New nucleic acid which alters flower morphology - by suppressing petals
PT and stamen(s), or converts them to other organs, partic. to produce
PT transgenic plants less susceptible to insect pests.
XX
PS Disclosure; Fig 1A; 33pp; English.
XX
CC A flower specific gene fbpl was isolated from the genome of Petunia
CC hybrida. This gene has the features of a transcription factor and belongs
CC to the group of MADS box genes. The fbpl gene is only active during
CC differentiation of floral organ primordia and plays a crucial role in the
CC determination of part of the floral meristem into petals and stamen
CC primordia. Plants transformed with the gene are less attractive to insect
CC pests so have better resistance to them; specifically cucumber plants are
CC protected against Frankliniella occidentalis but the method can be used
CC for other, esp. parthenocarpic and/or apomictic plants. The plants are
CC also less susceptible to secondary fungal infection. Elimination of
CC petals may improve photosynthesis and seed yield may be increased. See
CC also AAG55090-3. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 16-OCT-2003 to standardise OS field)
XX
SQ Sequence 780 BP; 277 A; 120 C; 172 G; 211 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 9,45e-62 Length: 780
Score: 684.50 Matches: 134
Percent Similarity: 82.33% Conservative: 43
Best Local Similarity: 62.33% Mismatches: 33
Query Match: 62.06% Indels: 5
Gaps: 2
US-10-069-527-2 (1-215) x AAG55089 (1-780)
QY 1 MetGlyTyrGlyGlyValGluIleValArgIleGluAsnSerSerAsnArgIValThr 20
DB 8 ATGGGGAGAGAAAGATGAGATGATAAAGATAGAAAACCAAGCAACACAGCAAGTACT 67
QY 21 TySerIysArgArgAngIyleIleIleLysLysAlaLysGluIleThrValIleCysAsp 40
DB 68 TACTCAAAAGAGAAATGGATGCTTGAATAAAAGCTAAGAAATTAAGTCTTCTTGAT 127
QY 41 AlAlaLysValSerIleIleIleTySerSerSerGlyLysMetValGluTyCysSerPro 60
DB 128 GCTGCTGTTCTGATCATCTTTGCTGAGCTGCGAAGATGATGATGATC-----TCN 181
QY 61 SerThrIleuThrIleuIleLysAspLysTyHisGlyIleGlnSerGlyLysLysLeuTrp 80
DB 182 TCTACTCTGTTGCTGATATTGATGATCAATATACAAAGCTTACTGTTAAGAAATGTTG 241
QY 81 AspAlaLysHisGluAsnLeuSerAsnGluValAspArgValIleLysIlyAspAsnAspSer 100
DB 242 GATGCTAAGCATGAGAACTTGACATGAATCAACAAGTCAAGAAAGACAAATGACAAAC 301
QY 101 MetGluValGluLeuArgHisIleLeuGlyGluAspIleIleHisSerLeuAsnHisValGlu 120
DB 302 ATGCAAAATTTGAACCTGAGCACTTGAAAGGTGAAATATCATCTTTGAACCAATGAGAG 361
QY 121 LeuMetAlaLeuGluGluAlaLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer 140
DB 362 CTGATGATATTGAAAGATGCCCTTGAATAATGAGCACTAGTATGTTCTTAACAAACAGAT 421
QY 141 LysHeValaIleMetMetArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeu 160
DB 422 GAGGTTCTGAGAGATGAGGAAAAAGACTTAAAGTATGAGAGGAGGACCAACCACTT 481
QY 161 ThrTyrgluLeuGlnIleGlnIleMetCysIleLysGluLeuValIleAspMetGlu 180
DB 482 AATTGCCAATTGGCCCAACTTGAGATGACAAACATGAAATATGGAATATGGGAAATTTGCC 541
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QY 181 AenGlyTyHisGlnArgGlnLeuGlyAsnTyHisAsnAsnGlnGlnIleProPhe 200
DB 542 GAAAGTCTTACGACAGAGGAGAGAAATGATGATCAACCAAAACCAT-----ATGCTTTT 592
QY 201 AlaPheArgValGlnProIleGlnProAsnLeuGlnGluAlaGlle 215
DB 593 GCCTTCGAGTACAAACCAATGACGCAAAATTTGACGAGAGAGTTG 637
RESULT 3
ADD55880
ID ADD55880 standard; cDNA; 896 BP.
XX
AC ADD55880;
XX
DT 15-JAN-2004 (first entry)
XX
DE Thalecress environmental stress-related cDNA #127.
XX
KW Thalecress; environmental stress; ss; plant; viral infection;
KW fungal infection; microbial infection; herbicide resistance; heat; cold;
KW heavy metal; low light; drought; osmotic stress; salt concentration;
KW transgenic.
XX
OS Arabidopsis thaliana.
XX
PN US2003131386-A1.
XX
PD 10-JUL-2003.
XX
PF 22-OCT-2002; 2002US-00278536.
XX
PR 23-MAR-1999; 99US-0125814P.
XX
PR 22-MAR-2000; 2000US-00532591.
XX
PA (SAMA/) SAMARA R.
PA (HEAR/) HEARD J.
PA (JIANG/) JIANG C.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER L.
PA (RIE/) RIECHMANN J L.
PA (YUG/) YU G.
PA (KED/) KEDDIE J.
PA (RATC/) RATCLIFFE O.
PA (PILG/) PILGRIM M.
PA (ADAM/) ADAM L.
PA (BROU/) BROUN P.
PA (ZHAN/) ZHANG J.
PI Samaha R, Heard J, Jiang C, Pineda O, Reuber L, Riechmann JL;
PI Yu G, Keddie J, Ratcliffe O, Pilgrim M, Adam L, Brown P, Zhang J;
DR WPI: 2003-829608/77.
XX
PT New recombinant polynucleotide for altering the regulation of gene
PT expression of plants to modify the plant's traits, particularly the
PT plant's environmental stress tolerance.
XX
PS Claim 14; SEQ ID NO 238; 219pp; English.
XX
CC The invention relates to a recombinant polynucleotide that alters a
CC plant's environmental stress tolerance when compared with the same trait
CC of another plant lacking the recombinant polynucleotide. Also included
CC are a transgenic plant comprising the novel recombinant polynucleotide
CC having a sequence that encodes a polypeptide comprising at least 6
CC consecutive amino acids of any of the 55 250-500 residue amino acid
CC sequences (S1), given in the specification, altering the environmental
CC stress response or tolerance of a plant, or altering a plant's trait and
CC altering the expression levels of at least one gene in a plant. The
CC recombinant polynucleotide and methods are useful for altering the
CC regulation of gene expression of plants to modify the plant's traits, in
CC particular with respect to environmental stress responses (e.g. to viral
CC infection, fungal infection, microbial infection, herbicide resistance,
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PR 29-JUN-1999; 99US-0140991P.
 PR 30-JUN-1999; 99US-0141287P.
 PR 01-JUL-1999; 99US-0141842P.
 PR 01-JUL-1999; 99US-0142154P.
 PR 02-JUL-1999; 99US-0142055P.
 PR 06-JUL-1999; 99US-0142350P.
 PR 08-JUL-1999; 99US-0142803P.
 PR 09-JUL-1999; 99US-0142920P.
 PR 12-JUL-1999; 99US-0142977P.
 PR 13-JUL-1999; 99US-0143542P.
 PR 14-JUL-1999; 99US-0143624P.
 PR 15-JUL-1999; 99US-0144005P.
 PR 16-JUL-1999; 99US-0144085P.
 PR 16-JUL-1999; 99US-0144086P.
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 PR 28-JUL-1999; 99US-0145951P.
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 PR 09-AUG-1999; 99US-0147493P.
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 PR 18-AUG-1999; 99US-0149426P.
 PR 20-AUG-1999; 99US-0149722P.
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 PR 31-AUG-1999; 99US-0151930P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0155070P.

PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
 PR 16-SEP-1999; 99US-0154039P.
 PR 20-SEP-1999; 99US-0154479P.
 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-0155659P.
 PR 28-SEP-1999; 99US-0156458P.
 PR 29-SEP-1999; 99US-0156596P.
 PR 04-OCT-1999; 99US-0157117P.
 PR 05-OCT-1999; 99US-0157753P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158025P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
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 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
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 PR 25-OCT-1999; 99US-0161405P.
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 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161933P.
 PR 29-OCT-1999; 99US-0162142P.

Alignment Scores:
 Pred. No.: 3,74e-59 Length: 947
 Score: 660.50 Matches: 130
 Percent Similarity: 75.81 Conservative: 33
 Best Local Similarity: 60.47 Mismatches: 39
 Query Match: 59.88 Indels: 13
 DB: 3 Gaps: 2

US-10-069-527-2 (1-215) x AAC39436 (1-947)

QY 1 MetGlyARGLylyValAluilelysaRglllegluansSerSerAsnArglnValThr 20
 122 ATGGGTAGAGGAAGATCGAGATTAAGAGATAGAGAGCAAGCAAGAGATGTGAG 181
 QY 21 TySerlyeARyARsnglyllelylsySAlyeGluileThyValleucysaP 40
 182 TTCTCAAGAGAGAGATGATTTGGAGAGAGCTTAAGAAATACAGATTCTTTGTGAT 241
 QY 41 AlaLyValserleullellelyrSerSerSerglyLysMetValGlnTyrcysSerP 60
 242 GCAAAAGTTCCTCATTAATCTTTCAGAGTAATGTAAGATGATTAATCACTGTTGCTCT 301
 QY 61 SerThrThreThrcJuleleuAspLyTyRHISGLyGlnSerGlyLysTySerP 80
 302 TCCATGATCTTGCTGCTATGTTGACCAATCCAGAACTTATCTGGCAAGAACTATAG 361
 QY 81 AspAlaLyHISGLyAsnLeuSerSerSerglyLysAspArgVallyLysAspAsnS 100
 362 GATGCTAAGCATAGAACTTGAACATGAGATTGATGATCAAGAAAGATGATAGC 421

QY 101 MetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu 120
 Db 422 TTTCACTGAGAGCTCAGGCTTTGAAAGGAGAAATATACATCTTCAACTTGAATAAT 481
 QY 121 LeuMetAlaLeuGlnGluAlaLeuGlnLysGlnGluThrSerLeuArgAspLysGlnSer 140
 Db 482 CTATGAGCTCTCAGAGCAGCGCATTTGAACATGGCTCGAAGAGTCCGAAACACCAAGAGATG 541
 QY 141 LysPheValAspMetLeuArgAspAsnGlyValAlaLeuGlnAspLysGlnLysArgLeu 160
 Db 542 GAGATCTCTATATCAAGAGAGAAATGAGAAATGATGCGGAGGAGCAAGCGCAATCTC 601
 QY 161 ThrTyrGlnLeuGlnLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
 Db 602 ACTTCCAGCTGCA---CAGCAGGAGATGGCTATGACAGCAAGCAGGAGATGAG 658
 QY 181 AsnGlyTyrHisGlnArgGlnLeuGlnLysArgTyrAsnAsnAsnGlnGlnGlnGln 200
 Db 659 ATGAGAGATCATATGAGGAG---TTT 682
 QY 201 AlapheArgValGlnProIleGlnProAsnLeuGlnGlnGlnGlnGlnGlnGlnGln 215
 Db 683 GATATATGAGTCAACGAGTTCAGCCAAATCTTCAAGAAAGATT 727
 RESULT 5
 ABR82089 standard; cDNA; 764 BP.
 AC ABR82089;
 DT 27-AUG-2002 (first entry)
 DE Novel floral meristem identity gene LpMADS1 contig #4.
 XX Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KM CEN-like protein; APERIALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KM inflorescence development; flower development; embryo development;
 KM hybrid seed production; herbage quality; early maturing crop;
 KM biomass increase; branching increase; blocking flowering;
 KM allergenic pollen; floral meristem identity protein; ss.
 XX Lolium perenne.
 OS
 XX
 PN W0200233091-A1.
 XX
 PD 25-APR-2002.
 XX
 PF 17-OCT-2001; 2001WO-AU001311.
 XX
 PR 19-OCT-2000; 2000AU-00000873.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 PI Sengenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX WPI; 2002-454601/48.
 DR
 XX
 PT New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APERIALA2, Homeo-box proteins, isolated from ryegrass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 XX
 PS Claim 3; Fig 29; 290pp; English.
 CC The invention describes a substantially purified or isolated polypeptide
 CC (1) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APERIALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
 CC and HB-like proteins, or their functionally active fragments or variants.

CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced bushiness in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence represents a contig
 CC polynucleotide novel floral meristem identity protein involved in floral
 CC development and a potential target for manipulating plant life cycles
 XX
 SQ Sequence 764 BP; 225 A; 202 C; 206 G; 129 T; 0 U; 2 Other;
 Alignment Scores:
 Pred. No.: 3,52e-58 Length: 764
 Score: 650.00 Matches: 122
 Percent Similarity: 77.00% Conservative: 42
 Best Local Similarity: 57.28% Mismatches: 43
 Query Match: 58.93% Indels: 6
 DB: Gaps: 2
 US-10-069-527-2 (1-215) x ABR82089 (1-764)
 QY 1 MetGlnValGlnLysValGlnLysValGlnLysValGlnLysValGlnLysValGlnLys 20
 Db 84 ATGGGGGGGGGAGAGATCGATCAAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 143
 QY 21 TyrSerLysArgArgAsnGlyIleIleLysValAlaLysGlnLysValLysValLysVal 40
 Db 144 TTCTCCAAAGGCAAGAGAGAGATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 203
 QY 41 AlaLysValSerLeuIleIleTyrSerSerSerGlyLysMetValGlnTyrCysSerPro 60
 Db 204 GCCGAGGTCCGCGCGCTCTCTCCAGCGCGGCAAGCTCTACAGCTCTCTCTCTCTCTCT 263
 QY 61 SerThrThrLeuThrGlnLysLeuAspLysTyrHisGlyGlnSerGlyLysLysLeuTrp 80
 Db 264 AAGACATCGCTATCAAGATCTTGGAGAGATACCAAGCAACTCCGGAGAGATCTGTGG 323
 QY 81 AspAlaLysHisLeuSerLeuSerAsnGlyValAlaAspArgValLysLysAspAspSer 100
 Db 324 GATGAGAAACAAAGAGCTCAGCGCGGAGATGATGATGATGATGATGATGATGATGATG 383
 QY 101 MetGlnValGlnLysValGlnLysValGlnLysValGlnLysValGlnLysValGlnLys 120
 Db 384 ATGCAAGATGAGAGCTCAGGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 443
 QY 121 LeuMetAlaLeuGlnGlnLysGlnGlnLysGlnGlnLysGlnGlnLysGlnGlnLysGln 140
 Db 444 TTGATCATGATGAG 503
 QY 141 LysPheValAspMetLeuArgAspAsnGlyValAlaLeuGlnAspLysGlnLysArgLeu 160
 Db 504 GAGACATCAACAGAGCTGATGAAATCGGAAAGATCTGAAAGATGAAAGATGAAAGATG 563
 QY 161 ThrTyrGlnLeuGlnLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
 Db 564 GCAATTTAAATCGAT---CAGCAAGATATTCGCTGAAAGAGAGAGAGAGAGAGAGAG 620

Oy ASG1TYPHI6LIngrngIneudlysnTyraenAenAnengIngInllleProPhe 200
Db 621 CTTGGTTCACATCCGCAGACG-----GACTTTGGAGGCCAGATGCGCATC 665

Oy 201 AlApheArYalGlInProIIecInProAsnleungInglu 213
Db 666 ACCTTCGGGTGCGCTTAGCCAGCCCAACCCTGCAGAGAG 704

RESULT 6
ABK82088
ID ABK82088 standard, cDNA, 783 BP.
XX
XX ABR82088;
DT 27-AUG-2002 (first entry)
DE Novel floral meristem identity gene LpmADS1 contig #3.

KM RRegras; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CN;
KM CN-Like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
KM HB-Like protein; plant growth; plant architecture;
KM inflorescence development; flower development; embryo development;
KM seed development; flower organ identity; phase change; male sterility;
KM hybrid seed production; herbage quality; early maturing crop;
KM biomass increase; branching increase; blocking flowering;
KM allegenic pollen; floral meristem identity protein; ss.

Os Lolium perenne.
Xs WO200233091-A1.
XX
XX PN 25-APR-2002.
PD
PF 17-OCT-2001, 2001WO-AU001311.
PP
PR 19-OCT-2000; 2000AU-00000873.
PX
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
PL Spangenberg G, Sawbridge TJ, Ong EK, Emmerling M;
DR WPI; 2002-454601/48.
XX
XX New substantially purified or isolated polypeptide e.g., MADS-box,
PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
PT fescue species, useful for controlling plant life cycles and/or growth
PT phases..
FI
FI Claim 3; Fig 29; 290pp; English.

The invention describes a substantially purified or isolated polypeptide
(I) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CN-Like
proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
and HB-Like proteins, or their functionally active fragments or variants
and Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
vector (IV) comprising (II), is useful for modifying plant life cycles
and/or growth phases, flowering processes, flowering and/or plant
architecture and/or flower and/or inflorescence development in a plant,
which involves introducing (II), (III) or (IV) into the plant. The
individual or simultaneous enhancement or downregulation of MADS-box gene
activities may alter flower, embryo and seed development, e.g., enhance
or inhibit embryo differentiation and growth or alter flower organ
identity through conversion of one floral organ in another. Manipulation
of CEN or HB activity in plants alters the control of phase change,
flowering time and the number of leaves made before flowering.
Manipulation of AP2 activity in plants alters flower organ identity
through conversion of one floral organ in another, leads to a change in
the number of floral organs and flowering architecture. Manipulation of
flowering plant architecture has a wide range of applications such as:
inducing male sterility for hybrid seed production; changing flower

CC	architecture for enhancing value of ornamentals; delaying flowering in forage grasses thus stopping the formation of less digestible stems and increasing herbage quality; altering flowering time allowing early maturing crops; delaying vegetative phase to increase biomass production; increasing branching to enhanced business in fruit trees; altering plant size e.g. shorter plant stature; and in blocking flowering and reducing release for allergenic pollen. This sequence represents a combi polynucleotide novel floral meristem identity protein involved in floral development and a potential target for manipulating plant life cycles
XX	Sequence 783 BP; 232 A; 204 C; 208 G; 138 T; 0 U; 1 Other;
5Q	
Alignment Scores:	
Pred. No.:	3,63e-58 Length: 783
Score:	650.00 Matches: 122
Percent Similarity:	77.00% Conservative: 42
Best Local Similarity:	57.28% Mismatches: 43
Query Match:	58.93% Indels: 6
DB:	Gaps: 2
US-10-069-527-2 (1-215) x ABRK82088 (1-783)	
QY	1 MetGlaYrGgLYlVsVaIgIuIlleYsArGtIlegIuSnSeSerSeAenArGInValThr 20
Db	78 AATGGGCGGGGAAAGTCAGATCAAGAGGATCGAAGCAACGAGCAACCCCGAGTACC 137
QY	21 TyrSerLYsArGArGsnGlyIlelleLYsLYsAlaLYsGluIleThrValleuCYsAsp 40
Db	138 TTCTCCAAAGCGCAAGACGGGATCCTCAAGAAAGCCAAAGAGATCAGCGTCTTGCGAC 197
QY	41 AlAlYsValSerleuIlelleYrSerSerSerGlyYSmEValGluYrCYsSerPro 60
Db	198 GCGGAGTGGGGCGTCTCTCTTCTCCAGCGCGGCAAGCTCTAGCACTTCTGCTCCCC 257
QY	61 SerThrThleuThrGluIleleuAspYrSYrYrISGLYGlInSerGlyLYsLYsLeuTyr 80
Db	258 AAGACATCGGTATCAAGATCTTGAGAAAGTACCAGACCACTCCGGGAAGATCTGTGG 317
QY	81 AspAlaLYsHISGLuSnleuSerSnGluValAspArGValYLYsYsAspAenAspSer 100
Db	318 GATGAGAAACACAAAGCGCTCAGCCGAGATGTATCAATCAAGAAAGAAATGATTAAC 377
QY	101 MetGluValGluIleuYrGHSleuLYsGlyIuAspIleThrSerleuAsnHISValGlu 120
Db	378 ATGCAGATCGAGCTCAGCACTTGAAAGCCAAAGATCGAATCACTGCAACCCAAAGAG 437
QY	121 leuMetAlaIeugIuIleuAlaIeugIuSnGlyLeuThrSerIleArGAspLYsGInSer 140
Db	438 TTGATCTGATATGAGGACACCTTATATATGACTGAGAGCGCTGATGAAGAACAGATG 497
QY	141 LYsPheValAspMetleuArGAspSnGlyLYsAlaIeugIuAspGlyAsnLYsArGLeu 160
Db	498 GAGCACTACGACAGGCTGTATGAAGAACTGGCAAGATGCTAGAAAGATGAGACAAATTGCTC 557
QY	161 ThrTYrGluIeugIuIuSnGInGluIuMetLYsIleLYsGluAsnValArGAspMetCglu 180
Db	558 GCATTTAAATCGAT---CAGCAAGATATTGGCTGGAACGGGAACAATGAGGAGACTTGAG 614
QY	181 AsnGlyYrYrHISGInArGInleuGlyAsnYrZnAsnAsnGInGInGInIleProPhe 200
Db	615 CTGGTTATCATCCGACAGG-----GACTTGCAGCCAGATGCCATC 655
QY	201 AlaPheArGValGInProIleGInProAenleuGInGlu 213
Db	660 ACGTTCGGGTGACGCTAGCCACCCCAACCTGCAGAG 698
RESULT 7	
ABR82085	
ID	ABR82085 standard; cDNA; 789 BP.
AC	
XX	ABR82085;
XX	
DT	27-AUG-2002 (first entry)

XX DNA encoding novel floral meristem identity protein *lpmADS1*.
 DE Ryegrass; fecuene; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 XX CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KM HB-like protein; plant growth; plant architecture; embryo development;
 KM inflorescence development; flower development; male sterility;
 KM seed development; flower organ identity; phase change; male sterility;
 KM hybrid seed production; herbage quality; early maturing crop;
 KM biomass increase; branching increase; blocking flowering;
 KM allergenic pollen; floral meristem identity protein; gene; ss.
 OS *Lolium perenne*.
 XX W0200233091-A1.
 XX 25-APR-2002.
 XX 17-OCT-2001; 2001WO-AU001311.
 XX 19-OCT-2000; 2000AU-00000873.
 XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 XX (AGRE-) AGRESEARCH LTD.
 XX Spangenberg G, Sawbridge TJ, Ong EK, Emmerling M;
 DR WPI; 2002-454501/48.
 DR P-PSDB; ABG60932.
 XX New substantially purified or isolated polypeptide e.g., MADS-box,
 PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from rye grass or
 PT fescue species, useful for controlling plant life cycles and/or growth
 PT phases.
 PS Claim 3; Fig 27; 290pp; English.
 XX The invention describes a substantially purified or isolated polypeptide
 CC (I) from a rye grass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
 CC MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
 CC proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB),
 CC and HB-like proteins, or their functionally active fragments or variants.
 CC Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
 CC vector (IV) comprising (II), is useful for modifying plant life cycles
 CC and/or growth phases, flowering processes, flowering and/or plant
 CC architecture and/or flower and/or inflorescence development in a plant,
 CC which involves introducing (II), (III) or (IV) into the plant. The
 CC individual or simultaneous enhancement or downregulation of MADS-box gene
 CC activities may alter flower, embryo and seed development, e.g., enhance
 CC or inhibit embryo differentiation and growth or alter flower organ
 CC identity through conversion of one floral organ in another. Manipulation
 CC of CEN or HB activity in plants alters the control of phase change,
 CC flowering time and the number of leaves made before flowering.
 CC Manipulation of AP2 activity in plants alters flower organ identity
 CC through conversion of one floral organ in another, leads to a change in
 CC the number of floral organs and flowering architecture. Manipulation of
 CC flowering plant architecture has a wide range of applications such as:
 CC inducing male sterility for hybrid seed production; changing flower
 CC architecture for enhancing value of ornamentals; delaying flowering in
 CC forage grasses thus stopping the formation of less digestible stems and
 CC increasing herbage quality; altering flowering time allowing early
 CC maturing crops; delaying vegetative phase to increase biomass production;
 CC increasing branching to enhanced biomass in fruit trees; altering plant
 CC size e.g. shorter plant stature; and in blocking flowering and reducing
 CC release for allergenic pollen. This sequence encodes a novel floral
 CC meristem identity protein involved in floral development and a potential
 CC target for manipulating plant life cycles
 XX Sequence 789 BP; 233 A; 207 C; 211 G; 138 T; 0 U; 0 Other.
 SQ
 Alignment Scores: 3.67e-58 Length: 789
 Pred. No.: 650.00 Matches: 122
 Score:

Percent Similarity: 77.00% Conservative: 42
 Best Local Similarity: 57.28% Mismatches: 43
 Query Match: 58.93% Indels: 6
 DB: 6 Gaps: 2
 US-10-069-527-2 (1-215) x ABK82085 (1-789)
 QY 1 MetGlyArgGlyLysValAlaGluIleLysArgIleGluAsnSerSerAsnArgGlnValThr 20
 DB ATGGGGCGCGGAGATCGAGATCAAGAGGATCAGAAACAGAGCAACCCCGAGGTGAC 143
 QY 21 TyrSerLysArgGlnGluIleLysValAlaGluIleLysValAlaGluIleLysValAlaGlu 40
 DB TTCTCCAGCGCGGAGATCGAGATCAAGAGGATCAGAAACAGAGCAACCCCGAGGTGAC 203
 QY 41 AlaLysValSerLeuIleLysValAlaGluIleLysValAlaGluIleLysValAlaGluIle 60
 DB GCCGAGGTGCGGCGGAGATCGAGATCAAGAGGATCAGAAACAGAGCAACCCCGAGGTGAC 263
 QY 61 SerThrThrLeuThrGluIleLysValAlaGluIleLysValAlaGluIleLysValAlaGlu 80
 DB 264 AAGACATCGCTTATCAAGATCTTGAGAGATGACCAACCTCCGGAGATATCTGTGG 323
 QY 81 AspAlaLysSerLeuIleLysValAlaGluIleLysValAlaGluIleLysValAlaGluIle 100
 DB 324 GATGAGAAACACAGAGATCGAGATCAAGAGGATCAGAAACAGAGCAACCCCGAGGTGAC 383
 QY 101 MetGlnValGluLeuArgHisLeuLysGlyGluAspIleThrSerLeuAsnHisValGlu 120
 DB 384 ATGCAGATCGAGCTGAGAGATCTTGAGAGATGACCAACCTCCGGAGATATCTGTGG 443
 QY 121 LeuMetLysLeuGluGluIleLysValAlaGluIleLysValAlaGluIleLysValAlaGlu 140
 DB 444 TTGATCATGATGAGAGATCTTGAGAGATGACCAACCTCCGGAGATATCTGTGG 503
 QY 141 LysPheValAspMetLeuArgAspAsnGlyLysAlaLeuGluAspGluAsnLysArgLeu 160
 DB 504 GAGCAGTACAGCAGAGCTGATGAAACCTGCAGAGATCTGAGAGATGAGAAACAGGTGAC 563
 QY 161 ThrThrProLeuGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180
 DB 564 GCATTAACTGCGAAT--CAGCAAGATATGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 620
 QY 181 AsnGlyThrHisGlnArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 200
 DB 621 CTGCTTACCATCGAG 665
 QY 201 AlaPheArgValGlnProIleGlnProAsnLeuGlnGln 213
 DB 666 ACGTTCCGCGTGCAGCTTACCAACCCCACTGACAGAG 704
 RESULT 8
 ID ABK82123 standard; cDNA, 979 BP.
 AC ABK82123;
 XX 27-AUG-2002 (first entry)
 DE DNA encoding novel floral meristem identity protein *lpmADS1*.
 XX Rye grass; fecuene; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
 KM CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
 KM HB-like protein; plant growth; plant architecture; embryo development;
 KM inflorescence development; flower development; male sterility;
 KM seed development; flower organ identity; phase change; male sterility;
 KM hybrid seed production; herbage quality; early maturing crop;
 KM biomass increase; branching increase; blocking flowering;
 KM allergenic pollen; floral meristem identity protein; gene; ss.
 OS *Lolium perenne*.
 XX W0200233091-A1.

XX 25-APR-2002.
XX 17-OCT-2001; 2001MO-AU001311.
XX 19-OCT-2000; 2000AU-00000873.
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
XX (AGRE-) AGRSEARCH LTD.
XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX WPI; 2002-454601/48.
XX P-PSDB; ABG60941.
XX New substantially purified or isolated polypeptide e.g., MADS-box,
XX CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
XX fescue species, useful for controlling plant life cycles and/or growth
XX phases.
XX Claim 3; Fig 54; 290pp; English.
XX The invention describes a substantially purified or isolated polypeptide
XX (i) from a ryegrass (*Lolium* sp.) or fescue (*Festuca* sp.) species, such as
XX MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
XX proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB)
XX and HB-like proteins, or their functionally active fragments or variants.
XX Nucleic acid (ii) encoding (i), a construct (iii) comprising (ii), or a
XX vector (iv) comprising (ii), is useful for modifying plant life cycles
XX and/or growth phases, flowering processes, flowering and/or plant
XX architecture and/or flower and/or inflorescence development in a plant,
XX which involves introducing (ii), (iii) or (iv) into the plant. The
XX individual or simultaneous enhancement or downregulation of MADS-box gene
XX activities may alter flower, embryo and seed development, e.g., enhance
XX or inhibit embryo differentiation and growth or alter flower organ
XX identity through conversion of one floral organ in another. Manipulation
XX of CEN or HB activity in plants alters the control of phase change,
XX flowering time and the number of leaves made before flowering.
XX Manipulation of AP2 activity in plants alters flower organ identity
XX through conversion of one floral organ in another, leads to a change in
XX the number of floral organs and flowering architecture. Manipulation of
XX flowering plant architecture has a wide range of applications such as:
XX inducing male sterility for hybrid seed production; changing flower
XX architecture for enhancing value of ornamentals; delaying flowering in
XX forage grasses thus stopping the formation of less digestible stems and
XX increasing herbage quality; altering flowering time allowing early
XX maturing crops; delaying vegetative phase to increase biomass production;
XX increasing branching to enhanced business in fruit trees; altering plant
XX size e.g. shorter plant stature; and in blocking flowering and reducing
XX release for allergenic pollen. This sequence encodes a novel floral
XX meristem identity protein involved in floral development and a potential
XX target for manipulating plant life cycles
XX SQ Sequence 979 BP; 305 A; 236 C; 246 G; 192 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 4.8e-58 Length: 979
XX Score: 650.00 Matches: 122
XX Percent Similarity: 77.00% Conservative: 42
XX Best Local Similarity: 57.28% Mismatches: 43
XX Query Match: 58.93% Indels: 6
XX DB: Gaps: 2
XX
XX US-10-069-527-2 (1-215) x ABK82123 (1-979)
XX QY 1 MetGtYAArGtGtYtValGtLleuYsArGtLleGtLleuSArSArGtLleValThr 20
XX DB 134 ATGGGGCCGGGGAAGATCGAGTCAAGAGATCGAGGAAACCGCAGGTGACC 193
XX QY 21 TysSerLYsArGArGAsnGlyLleLleLYsLYsAlaLYsGtLleThrValLeuCYsAsp 40
XX DB 194 TTCTCCAGCGCAAGAGCGGATCTCTCAAGAGGCGCAAGAGATCAGGTGCTGCGCAC 253

QY 41 AlalysValSerLleLleLYsSerSerSerGtLYsMetValGtLYsCYsSerPro 60
DB GCCGAGCTCGGCGCTGCTGCTCTCCAGCCCGCAAGCTCTACGACTTGTGCTCCCC 313
QY 61 SerThrThrLleuThnGtLleuAspLYsTYrHisGlyGlnSerGtLYsLYsLleuTrp 80
DB 314 AAGACATGCTATCAAGATCTTGGAGAGATCCAGACCAACTCCGGGAAATACTGTGG 373
QY 81 AspaLYsSHIsgLYsLleuSerAsnGtLYsValAspaLYsLYsAspaAsnAspSer 100
DB 374 GATGAGAAACCAAGAGCCTCAGCGCGGATGTCATCAAGAAAGAAATGATTAAC 433
QY 101 MetGtLYsAlGtLleuLYsHisLleuLYsGtLYsAspLleuThrSerLleuAsnHisValGtLY 120
DB 434 ATGCAGATCGAGCTCAGGACTTGAAAGCCGAAAGTCACTCACTCAACCCCAAGAG 493
QY 121 LeuMetAlaLleuGtLYsAlaLleuGtLYsAsnGtLYsThrSerLleuAspLYsGlnSer 140
DB 494 TTGATCATGATTTGAGGAAGCACTTATATGACTGACAGGCTGCTGCAAAAACAGATG 553
QY 141 LysPheValAspMetMetArgAspAsnGtLYsAlaLleuGtLYsAsnLYsArgLeu 160
DB 554 GAGCACTACGACAGGCTGATGAAACTGGCAAGATGTAGAGATGAGACAAAGTTGCTC 613
QY 161 ThrTYrGtLleuGtLYsGlnGtLYsLleuLYsLleuLYsGtLYsValAsnValArgAsnMetGtLY 180
DB 614 GCATTAACTGCAT---CAGCAAGATTTGGCGCTGAAACGGGAACATGAGGGAGCTTGAG 670
QY 181 AsnGtLYrHisGtLYsGtLYsGtLYsAsnTYrAsnAsnAsnGlnGtLYsLleuProPhe 200
DB 671 CTGGTTCATCATCCGACAGG-----GACTTGACAGCCCAAGTGCCTGATC 715
QY 201 AlaPheArgValGtLYsProLleGtLYsProAsnLleuGtLYs 213
DB 716 AGCTTCGGGTCAAGCTTACGACCCCAACCTGCGAGAG 754
XX
XX RESULT 9
XX ID ABK82124 standard; cDNA; 1065 BP.
XX AC ABK82124;
XX XX
XX 27-AUG-2002 (first entry)
XX DE
XX DNA encoding novel floral meristem identity protein LPMADS1b.
XX KW Ryegrass; fescue; MADS-box; MADS; MADS-like protein; CENTRORADIALIS; CEN;
XX CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
XX HB-like protein; plant growth; plant architecture;
XX inflorescence development; flower development; embryo development;
XX seed development; flower organ identity; phase change; male sterility;
XX hybrid seed production; herbage quality; early maturing crop;
XX biomass increase; branching increase; blocking flowering;
XX allergenic pollen; floral meristem identity protein; gene; ss.
XX KW
XX OS
XX Solium Perenne.
XX MO200233091-A1.
XX PN
XX 25-APR-2002.
XX PD
XX 17-OCT-2001; 2001MO-AU001311.
XX PF
XX 19-OCT-2000; 2000AU-00000873.
XX PR
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
XX PA (AGRE-) AGRSEARCH LTD.
XX XX
XX Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX WPI; 2002-454601/48.
XX DR P-PSDB; ABG60941.
XX XX

CC which involves introducing (II), (III) or (IV) into the plant. The
CC individual or simultaneous enhancement or downregulation of MADS-box gene
CC activities may alter flower, embryo and seed development, e.g., enhance
CC or inhibit embryo differentiation and growth or alter flower organ
CC identity through conversion of one floral organ in another. Manipulation
CC of CEN or HB activity in plants alters the control of phase change,
CC flowering time and the number of leaves made before flowering.
CC Manipulation of AP2 activity in plants alters flower organ identity
CC through conversion of one floral organ in another, leads to a change in
CC the number of floral organs and flowering architecture. Manipulation of
CC flowering plant architecture has a wide range of applications such as:
CC inducing male sterility for hybrid seed production; changing flower
CC architecture for enhancing value of ornamentals; delaying flowering in
CC forage grasses thus stopping the formation of less digestible stems and
CC increasing herbage quality; altering flowering time allowing early
CC maturing crops; delaying vegetative phase to increase biomass production;
CC increasing branching to enhanced biomass in fruit trees; altering plant
CC size e.g. shorter plant stature; and in blocking flowering and reducing
CC release for allergenic pollen. This sequence represents a contig
CC polynucleotide novel floral meristem identity protein involved in floral
CC development and a potential target for manipulating plant life cycles
XX
SQ Sequence 780 BP, 229 A; 203 C; 206 G; 136 T; 0 U; 6 Other;

Alignment Scores:
Pred. No.: 1,2e-57 Length: 780
Score: 645.00 Matches: 122
Percent Similarity: 76.53% Conservative: 41
Best Local Similarity: 57.28% Mismatches: 44
Query Match: 58.48% Indels: 6
DB: Gaps: 2

US-10-069-527-2 (1-215) x ABK82086 (1-780)

QY 1 MetGlyArgGlyValGluIleValArgIleGluAsnSerSerAsnArgIleValThr 20
DB 84 ATGGGGGCGTGGAGGATCGAGATCGAGATCGAGAACAGCAACCCCGAGGTGACC 143
QY 21 TySerIysArgArgAsnGlyIleIleValAlaLysGluIleThrValLeuCyasp 40
DB 144 TTCTCCAAAGCGCAAGAACGGGATCTCCAGAGGCCAAGAGATACGCTCTGGAC 203
QY 41 AlaIysValSerLeuIleIleIleTySerSerGlyLysMetValGluTyCySerPro 60
DB 204 GCCAGAGTCGGCGCTGCTCTCTCCAGCGCCGCGAAGCTCAACGCTCTCTCCCA 263
QY 61 SerThrThrLeuThrGluIleLeuAspLysTyThrIleGlyIleSerGlyLysLeuTrp 80
DB 264 AAGCAATCGCTATCAAGATCTTGAGACATGACAGCCAACTCCGGAGATACGTG 323
QY 81 AspAlaIysHisGluAsnLeuSerAsnGluValAspArgValLysIlyAspAsnSer 100
DB 324 GATAGAGAAACAACAAGCCTCAGTCGAGATTCATCAATCAAGAAAGAAATGACAC 383
QY 101 MetGluValGluLeuAspGlyIleValGluAspIleThrSerLeuAsnHisValGlu 120
DB 384 ATGCAAGATCGAGCTCAGGACCTTGAAAGCGCAAGATCTGAATCACTGCAACCAAG 443
QY 121 LeuMetAlaLeuGluGluIleValLeuAsnGlyLeuThrSerIleArgAspLysGlnSer 140
DB 444 TTGATCATGATTGAGAGACCTTGATATATGACTGACAGCCCTGCATGAAAAACATG 503
QY 141 LysIleValAspMetMetArgAspAsnGlyValAlaLeuGluAspGluValAspGlu 160
DB 504 GAGCACTACGACAGCGCGATGAAAACTGGCAAGATGCTAGAGATGAGAACAGTCTCTC 563
QY 161 ThrTyGluLeuGlnIleValGlnIleMetLysIleLysGluAsnValArgAsnMetGlu 180
DB 564 GCATCTAACTGCAT---CAGCAAGATATATGCGTGAACGGGAACATGAGGAGCTTGAG 620
QY 181 AsnGlyIleValGlnIleValGlnIleValAsnTyArgAsnAsnGlnIleProPhe 200
DB 621 CTTGGTAAACATCCGAGACAG---GACCTTGACGCCAGATGCGCATC 665

QY 201 AlaPheArgValGlnProIleGlnProAsnLeuGlnIle 213
DB 666 ACGTTCGCGTGCAGACCTAGCCACACCACCACTGCGAGG 704
RESULT 11
ABK82087
ID ABK82087 standard; cDNA; 783 BP.
XX
AC ABK82087;
XX
DT 27-AUG-2002 (first entry)
XX
DE Novel floral meristem identity gene LpMADS1 contig #2.
XX
KW Ryegrass; fescue; MADS-box; MADS-like protein; CENTRORADIALIS; CEN;
KW CEN-like protein; APETALA2; AP2; AP2-like protein; HB; Homeo-box protein;
KW HB-like protein; plant growth; plant architecture;
KW inflorescence development; flower development; embryo development;
KW seed development; flower organ identity; phase change; male sterility;
KW hybrid seed production; herbage quality; early maturing crop;
KW biomass increase; branching increase; blocking flowering;
KW allergenic pollen; floral meristem identity protein; ss.
XX
OS Lolium perenne.
XX
PN WO200233091-A1.
XX
PD 25-APR-2002.
XX
PF 17-OCT-2001; 2001WO-AU001311.
XX
PR 19-OCT-2000; 2000AU-00000873.
XX
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
XX
AB (AGRE-) AGRESEARCH LTD.
XX
PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
XX
DR WPI; 2002-454601/48.
XX
PT New substantially purified or isolated polypeptide e.g., MADS-box,
PT CENTRORADIALIS, APETALA2, Homeo-box proteins, isolated from ryegrass or
PT fescue species, useful for controlling plant life cycles and/or growth
PT phases.
XX
PS Claim 3; Fig 29; 290pp; English.
XX
XX
XX The invention describes a substantially purified or isolated polypeptide
XX (I) from a ryegrass (Lolium sp.) or fescue (Festuca sp.) species, such as
XX MADS-box (MADS) and MADS-like proteins, CENTRORADIALIS (CEN) and CEN-like
XX proteins, APETALA2 (AP2) and AP2-like proteins, Homeo-box proteins (HB),
XX and HB-like proteins, or their functionally active fragments or variants.
XX Nucleic acid (II) encoding (I), a construct (III) comprising (II), or a
XX vector (IV) comprising (II), is useful for modifying plant life cycles
XX and/or growth phases, flowering processes, flowering and/or plant
XX architecture and/or flower and/or inflorescence development in a plant,
XX which involves introducing (II), (III) or (IV) into the plant. The
XX individual or simultaneous enhancement or downregulation of MADS-box gene
XX activities may alter flower, embryo and seed development, e.g., enhance
XX or inhibit embryo differentiation and growth or alter flower organ
XX identity through conversion of one floral organ in another. Manipulation
XX of CEN or HB activity in plants alters the control of phase change,
XX flowering time and the number of leaves made before flowering.
XX Manipulation of AP2 activity in plants alters flower organ identity
XX through conversion of one floral organ in another, leads to a change in
XX the number of floral organs and flowering architecture. Manipulation of
XX flowering plant architecture has a wide range of applications such as:
XX inducing male sterility for hybrid seed production; changing flower
XX architecture for enhancing value of ornamentals; delaying flowering in
XX forage grasses thus stopping the formation of less digestible stems and
XX increasing herbage quality; altering flowering time allowing early
XX maturing crops; delaying vegetative phase to increase biomass production;


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PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144335P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144332P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 22-JUL-1999; 99US-0145088P.
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PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
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PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
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PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161982P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

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Alignment Scores:

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Pred. NO.: 6,11e-57 Length: 1004
Score: 639.50 Matches: 124
Percent Similarity: 76.53% Conservative: 39
Best Local Similarity: 58.22% Mismatches: 47
Query Match: 57.98% Indels: 3
DB: 3 Gaps: 2

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US-10-069-527-2 (1-215) x AAC46623 (1-1004)

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DB 163 ATGGGCGCGCGCAAGATCGAGATCGAGATCGAGAACTCTACCAACCGCGAGTGACC 222
QY 21 TySerLysArgArgAsnGlyIleIleLysLysAlaLysGluIleThrValLeuCyasp 40
DB 223 TTCTCCAAAGCGCGCGCGAGCTGATCGTCAAGACGCGAGATCGCGCTCGTCGAC 282
QY 41 AlaLysValSerLeuIleIleLysSerSerSerGlyLysMetValGluIleThrCyasp 60
DB 283 GCCGAGGTGGCGCGCGATCTTCTCCAGCGCGCAAGCTCTATGACTGCTGCGCC 342
QY 61 SerThrThrLeuThrGluIleLeuAspLysIleGlyGlnSerGlyLysLysLeuTrp 80
DB 343 AGGACCTCGCTGCCAGATCTTGGAGAGTACCAACCACTCCGGAGAGATTCGTGG 402
QY 81 AspAlaLysHisGluLeuLeuSerAsnGluValAspArgValLysLysAspAsnAspSer 100
DB 403 GGTGAGAGCAACAAGACCTGAGTGCAGATCGACAGTCAAGAGAGCAAGCAAC 462
QY 101 MetGluValGluLeuLeuArgHisLeuLysGlyLysAspIleThrSerLeuAsnHisValGlu 120
DB 463 ATGCAGATTCAAGCTCAAGCATCTGAAAGCGAGAGCACTGAACTCCCTGCAGCCAGAGAC 522
QY 121 LeuMetAlaLeuGluGluValLeuGluAsnGlyLeuThrSerIleArgAspLysGlnSer 140
DB 523 CTGATCGCTATTGTAAGAGGCGCTCCAGATGGCGCAACCACTCGCGCAAGAGCAGATG 582
QY 141 LysMetValAspMetMetArgAspAsnGlyLysAlaLeuGluAspGluLeuLysAspGlu 160
DB 583 GACTACTGGAGATGCACACGACCAATGGAGATGCTGAGAGCAACATTAAGATATCTG 642

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Alignment Scores:	2.87e-56
Pred. No.:	
Score:	632.50
Percent Similarity:	75.35%

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DB:	3	Gaps:	2			
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QY	1 MetGlyArgGlyIlyValGluIleIysArgIleGluSerSerAsnArgIleValThr	20				
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QY	21 TyrSerIlyArgArgGlnGlyIleIleIysIlyValIlyGluIleThrValIleCysAsp	40				
DB	144 TTCTCAAGGAGGAGATGATGATTGGGAAGAGGCTTAAGAAGATCAACGATCTTTTGAT	203				
QY	41 AlAlaValSerLeuIleIleTyrSerSerSerGlyIlyMetValGluTyrCysSerPro	60				
DB	204 GCAAAAGTTCCTCATATCTTTGCGAGTAAAGTAAAGATGATGATTAATCTGTGTCT	265				
QY	61 SerThrThrLeuThrGluIleLeuAspIlyTyrIleGlyIleSerGlyIlyValLeuThr	80				
DB	264 TCCATGGATTTGGTCTGTTGTTGGACCATCCAGAAATTATCTGGCAC-AAACTATGG	322				
QY	81 AspAlaIlySerIlyGluSerLeuSerAsnGluValAspArgValIlyLysAspAsnAspSer	100				
DB	323 GATGCTTAGATAGAACCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATG	382				
QY	101 MetGluValGluLeuArgIlyIleuIlySerGlyIlyAspIleThrSerLeuAsnHisValGlu	120				
DB	383 TTCAACTGGAGCTCGCATTTGAAGGAGAGATATACAGCTCTCAACTGAAAAAT	442				
QY	121 LeuMetAlaLeuGluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu	140				
DB	443 CTGATGCTGTCCAGACCGCATTAAGCACTGGCTTCGCAAAATGCCAGACACCAATG	502				
QY	141 LysPheValAspMetMetArgAspAsnGlyIlyValAlaLeuGluIlyAsnIlyArgLeu	160				
DB	503 GAGATCCTTATATCAAAAAGAGAAATAGAGAAATGATGGCGGAGAGCAACGGCACTC	562				
QY	161 ThrTyrGluLeuGluIlySerGlnGluMetIlyIleIysGluAsnValArgAsnMetGlu	180				
DB	563 ACTTTCACAGCTGCA---CAACAGAGATGCTTATAGCAACACGCAAGGAGATATG	619				
QY	181 AsnGlyTyrIleIleGlnArgIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu	200				
DB	620 ATGAGAGATCATATGCGCAG-----TTT	643				
QY	201 AlaPheArgValGlnProIleGlnProAsnLeuGlnIlyArgIle	215				
DB	644 GGATATAGAGTGCACCGCATTCACGCAAAATCTTCAGAAAAAGATT	688				
RESULT 15						
AAD42258						
ID	AAD42258 standard; cDNA, 1089 BP.					
XX	AAC					
DT	04-NOV-2002 (first entry)					
XX	Corn AP3 homologue cDNA from clone cmlc.pK002.j23.					
DE						
XX	Floral developmental protein; flowering locus T; APETALA3; transgenic;					
KW	FT; A3; transgenic plant; fertility; flower development; gene mapping;					
KW	sterility; plant growth; inflorescence architecture; plant morphology;					
KW	tissue culture; cell division; corn; gene; ss.					
XX						
OS	Zea mays.					
XX						
XX	Key					
FT	Location/Qualifiers					
FT	120..749					
FT	/*tag= a					
FT	/product= "Corn AP3 homologue protein"					
XX						
FN	W0200244390-A2.					

